

(A) NAME/KEY: other
(B) LOCATION: 17..162
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 110..255
id T82829
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..162
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..147
id AA027213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..162
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 2..132
id AA095731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 179..216
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 149..186
id AA095731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(85..162)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 358..435
id AA027214
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(16..87)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 434..505
id AA027214
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 37..84
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.3
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

CTTTTTTACT TTCACAGCAA TAGTGCAGAA TCCAGA ATG GAT GTC CTC TTT GTA      54
                               Met Asp Val Leu Phe Val
                               -15

GCC ATC TTT GCT GTG CCA CTT ATC CTG GGA CAA GAA TAT GAG GAT GAA      102
Ala Ile Phe Ala Val Pro Leu Ile Leu Gly Gln Glu Tyr Glu Asp Glu
-10                               -5                               1                               5

GAA AGA CTG GGA GAG GAT GAA TAT TAT CAG GTG GTC TAT TAT TAT ACA      150
Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln Val Val Tyr Tyr Tyr Thr
                               10                               15                               20

GTC ACC CCC ATT ATG ATG RCY TTA GGG MCR RAT TTC ACC ATT GAT TAC      198
Val Thr Pro Ile Met Met Xaa Leu Gly Xaa Xaa Phe Thr Ile Asp Tyr
                               25                               30                               35

KCC ATA TTT GAG TCA GAG                                          216
Xaa Ile Phe Glu Ser Glu
40

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 3..181
id N27605
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..53)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..51
id N78549
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3

seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

AAACTCCACG GCTGTGAAG ATG GCG GCT GCT GCG TGG CTT CAG GTG TTG CCT	52
Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro	
-20 -15	
GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA CCA CTG TCG TTT TTC	100
Val Ile Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe	
-10 -5 1 5	
AGT GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC CGG TCC AAA TGG CAC	148
Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His	
10 15 20	
ATT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT TTT GGA AAG ATC CTC	196
Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu	
25 30 35	
TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT GGA GAA CCT TGT GAC	244
Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp	
40 45 50	
CTG TCT TTG AAT ATA ACC TGG TAT CTG AAA AGC GCT GAT TGT TAC AAT	292
Leu Ser Leu Asn Ile Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn	
55 60 65 70	
GAA ATC TAT AAC TTC AAG GCA GAA GAA GTA GAG TTG TAT TTG GAA AAA	340
Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys	
75 80 85	
CTT	343
Leu	

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 72..267
id R13448
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 126..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 82..211
id T69236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 79..126
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 36..83
id T69236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..244
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 73..269
id R12437
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..211
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 136..299
id HSC1WH101
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..34
id HSC1WH101
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..150
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq LLXLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AGCGTTTTCH GSCCGTGCGT TTGTGGCGGT CCGGCCTCCC TGACATGCAG CCCTCTGGAC 60

CCCGAGGTTG GACCCTACTG TGACACACCT ACC ATG CGG ACA CTC TTC AAC CTC 114

Met Arg Thr Leu Phe Asn Leu


```

CTC TKG CTT GCC CTG GCC TGC AGC CCT GTT CAC ACT ACC CTG TCA AAG      162
Leu Xaa Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys
      -10                      -5                      1

TCA GAT GCC AAA AAA GCC GCC TCA AAG ACG CTG CTG GAG AAG AGT CAG      210
Ser Asp Ala Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln
      5                      10                      15                      20

TTT TCA GAT AAG CCG GTG CAA GAC CGG GGT TTG GTG GTG ACG GAC GGG      258
Phe Ser Asp Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Gly
      25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 8..198
id R72126
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 8..175
id W60037
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..174
id W24729
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 228..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 209..252
id W24729
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..174
id R74426
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 228..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 209..252
id R74426
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..174
id H42031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 228..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 209..252
id H42031
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..181
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9
seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```
ACTGAAGTGG GCAAATCCC CGAGAAGCAG CGGTGTCCCC AGCCTCTCAC TCGGAGCCGA    60
T  ATG GGG AGT AAA GTG GCG GAC CTG CTG TAC TGG AAG GAC ACG AGG ACG    109
Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
-40                -35                -30                -25

TCA GGA GTG GTC TTC ACA GGC CTG ATG GTC TCC CTC CTC TGC CTC CTG    157
Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
-20                -15                -10

CAC TTT AGC ATC GTG TCC GTG GCC GCG SAC TTT GGS YCK KKT DSY WGM    205
```

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa
-5 1 5

YTK GGG GMA CAA TCC TCT YTC AGG GTT TAC GCA AAG TGC TGC AGG CCG 253
Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro
10 15 20

TGC ACC GGG GGG ATG GAG 271
Cys Thr Gly Gly Met Glu
25 30

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 14..114
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 111..176
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 174..240
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..195
id AA206940

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 35..229
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..195
 id AA186993
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 37..229
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..193
 id T68050
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 32..178
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..147
 id AA157180
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 175..231
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 146..202
 id AA157180
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 28..114
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.9
 seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TCACTTATAG AAGGGAGAGG AGCGAAC ATG GCA GCG CGT TGG CGG TTT TGG TGT	54
Met Ala Ala Arg Trp Arg Phe Trp Cys	
-25	
GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC GTT TGC GAC GTT CCC	102
Val Ser Val Thr Met Val Val Ala Leu Leu Ile Val Cys Asp Val Pro	
-20 -15 -10 -5	
TCA GCC TCT GCC CAA AGA AAG AAG GAG ATG GTG TTA TCT GAA AAG GTT	150
Ser Ala Ser Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val	
1 5 10	
AGT CAG CTG ATG GAA TGG ACT AAC AAA AGA CCT GTA ATA AGA ATG AAT	198

Ser Gln Leu Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn
15 20 25 234
GGA GAC AAG TTC CGT CGC CTT GTG AAG CCC CAC ATG
Gly Asp Lys Phe Arg Arg Leu Val Lys Pro His Met
30 35 40

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 186..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..81
id AA089592
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 81..127
id AA089592
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 385..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..224
id AA089592
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(305..440)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 211..346
id R83736
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(294..439)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 202..347
 id R83667
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..86
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.8
 seq SAVLSGFVLGALA/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

AACTCTTG TG TAGCCTGAGG CGGCGGTAS ATG GAG GGG GAG AGT ACG TCG GCG      53
                               Met Glu Gly Glu Ser Thr Ser Ala
                               -15

GTG CTC TCG GGC TTT GTG CTC GGC GCA CTC GCT TTC CAG CAC CTC AAC      101
Val Leu Ser Gly Phe Val Leu Gly Ala Leu Ala Phe Gln His Leu Asn
-10                               -5                               1                               5

ACG GAC TCG GAC ACG GAA GGT TTT CTT CTT GGG GAA GTA AAA GGT GAA      149
Thr Asp Ser Asp Thr Glu Gly Phe Leu Leu Gly Glu Val Lys Gly Glu
                               10                               15                               20

GCC AAG AAC AGC ATT ACT GAT TCC CAA ATG GAT GAT GTT GAA GTT GTT      197
Ala Lys Asn Ser Ile Thr Asp Ser Gln Met Asp Asp Val Glu Val Val
                               25                               30                               35

TAT ACA ATT GAC ATT CAG AAA TAT ATT CCA TGC TAT CAG CTT TTT AGC      245
Tyr Thr Ile Asp Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser
                               40                               45                               50

TTT TAT AAT TCT TCA GGC GAA GTA AAT GAG CAA GCA CTG AAG AAA ATA      293
Phe Tyr Asn Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile
                               55                               60                               65

TTA TCA AAT GTC AAA AAG AAT GTG GTA GGT TGG TAC AAA TTC CGT CGT      341
Leu Ser Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg
                               70                               75                               80                               85

CAT TCA GAT CAG ATC ATG ACG TTT AGA GAG AGG YTG CTT CAC AAA AAC      389
His Ser Asp Gln Ile Met Thr Phe Arg Glu Arg Leu Leu His Lys Asn
                               90                               95                               100

TTG CAG GAG CAT TTT TCA AAC CAA GAC CTT GTT TTT CTG CTA TTA ACA      437
Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu Thr
                               105                               110                               115

CCA                                                                 440
Pro

```

(2) INFORMATION FOR SEQ ID NO: 134:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 45..258
id H81225
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..39
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..38
id H81225
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..216
id AA044118
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..225
id W01412
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 13..226
id W42797
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 95..230
id R39635
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 15..94
id R39635
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..201
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

AAAGTGAGTT AAGGACGTAC TCGTCTTGGT GAGAGCGTGA STGCTGAGAT TTGGGAGTCT      60
GCGCTAGGCC CGCTTGGAGT TCTGAGCCGA TGGAAGAGTT CACTC ATG TTT GCA CCC      117
                                         Met Phe Ala Pro
                                         -30

GCG GTG ATG CGT GCT TTT CGC AAG AAC AAG ACT CTC GGC TAT GGA GTC      165
Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
-25                                -20                                -15

CCC ATG TTG TTG CTG ATT GTT GGA GGT TCT TTT GGT CTT CGT GAG TTT      213
Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe
-10                                -5                                1

TCT CAA ATC CGA TAT GAT GCT GTG AAG AGT AAA ATG GAT CCT GAG CGG      261
Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Arg
5                                10                                15                                20

```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 143..345
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 113..315
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 335..442
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 304..411
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 43..120
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 44..317
id HUM172D06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 372..442
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 340..410
id HUM172D06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..73
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 8..46
id HUM172D06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 153..442
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 125..414
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 77..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..119
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..412
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 45..385
id HUM159G08B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..73
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..47
id HUM159G08B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 143..367
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 92..316
id N34957
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 80..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 30..97
id N34957
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 362..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 312..379
id N34957
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..431
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.7
seq AVALSLFLGWLGA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

AAGAGAAAGT GTCGGTCTCC AAG ATG GCG GCC GCC TGG CSD TCT GGT CCG TCT    53
               Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser
               -135                      -130

GCT CCG GAG GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC    101
Ala Pro Glu Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val
-125                      -120                      -115

TCA GTC ACT ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC    149
Ser Val Thr Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly
-110                      -105                      -100                      -95

GAG GAG TCG CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT    197
Glu Glu Ser Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys
-90                      -85                      -80

AAA GAT CCA AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA    245
Lys Asp Pro Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr
-75                      -70                      -65

AAC TAC ACA GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT    293
Asn Tyr Thr Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys
-60                      -55                      -50

AAG GAT TCC AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT    341
Lys Asp Ser Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly
-45                      -40                      -35

TTT TTC AAG CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC AAA    389
Phe Phe Lys Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys
-30                      -25                      -20                      -15

GTG GCA GTC GCA TTG TCT CTT TTT CTT GGA TGG TTG GGA GCA GAT CGA    437
Val Ala Val Ala Leu Ser Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg
-10                      -5                      1

TTT                                                                440
Phe

```

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..165
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

```
region 136..274
id HSC1WH101
est
```

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 73..211
id R12437
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 72..210
id R13448
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 73..129
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq LLWLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTGGCCGTC	CGGCCTCNCT	GACATGCAGC	CCTCTGGACC	CCGAGGTTGG	ACCCTACTGT	60
GACACACCTA	CC ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC	111				
	Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala					
	-15 -10					
TGC AGC CCT GTT CAC ACT ACC CTG TCA AAG TCA GAT GCC AAA AAA GCC	159					
Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala						
-5 1 5 10						
ACC TCA GGG	168					

Thr Ser Gly

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..381
id C15922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 224..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 200..328
id AA100508
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..225
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 96..200
id AA100508
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..90
id AA100508
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..353
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 89..421
id W27023

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 353..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 422..463
id W27023
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 76..245
id W68781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 267..361
id W68781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..69
id W68781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 101..331
id T80234
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 62..102
id T80234
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..37
id T80234
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 132..257
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq ASLFLLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

AAGAGGAGAC TGCAGACTTC GGTGAGGAA ACGGGTATTT CATGTCTCAG GGAGTAGGTT      60
TGTCAGTTA CAGCTTTTCT GTTGGTATGC ATAATTAATA ATTGGAGCTG CAAAGCAGAT    120
CGTGACAAGA G ATG GAC GGT CAG AAG AAA AAT TGG AAG GAC AAG GTT GTT      170
           Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val
           -40                               -35                               -30

GAC CTC CTG TAC TGG AGA GAC ATT AAG AAG ACT GGA GTG GTG TTT GGT      218
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
           -25                               -20                               -15

GCC AGC CTA TTC CTG CTG CTT TCA TTG ACA GTA TTC AGC ATT GTG AGC      266
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
           -10                               -5                               1

GTA ACA GCC TAC ATT GCC TTG GCC CTG CTC TCT GTG ACC ATC AGC TTT      314
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
           5                               10                               15

AGG ATA TAC AAG GGT GTG ATC CAA GCT ATC CAG AAA TCA GAT GAA GGC      362
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
           20                               25                               30                               35

CAC CCA TTC AGG GCA TAT CTG GAA TCT GAA GTT GCT ATA TCT      404
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser
           40                               45

```

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 439..475

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 24..60
 id AA013254
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 41..94
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.5
 seq LVLGLVLPILWA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

AACTTTCCCA GTCCTAGGCG GCGGTCAGAT CCTTGCAAGC ATG GTC GCG CCG GGG      55
                                     Met Val Ala Pro Gly
                                     -15

CTT GTA CTC GGG CTG GTG CTG CCA TTA ATC CTG TGG GCC GAC AGA AGT      103
Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu Trp Ala Asp Arg Ser
-10                               -5                               1

GCA GGT ATT GGT TTT CGC TTT GCT TCA TAC ATC AAT AAT GAT ATG GTG      151
Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile Asn Asn Asp Met Val
  5                               10                               15

CTG CAG AAG GAG CCT GCT GGG GCA GTG ATA TGG GGC TTC GGT ACA CCT      199
Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp Gly Phe Gly Thr Pro
  20                               25                               30                               35

GGA GCC ACA GTG ACC GTG ACC CTG CGC CAA GGT CAG GAA ACC ATC ATG      247
Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly Gln Glu Thr Ile Met
                               40                               45                               50

AAG AAA GTG ACC AGT GTG AAA GCT CAC TCT GAT ACG TGG ATG GTG GTA      295
Lys Lys Val Thr Ser Val Lys Ala His Ser Asp Thr Trp Met Val Val
                               55                               60                               65

CTG GAT CCT ATG AAG CCT GGA GGR SCT TTC GAA GTG ATG GCA CAA CAG      343
Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu Val Met Ala Gln Gln
  70                               75                               80

ACT TTG GAG AAA ATA AAC TTC ACC CTG AGA GTT CAT GAC GTC CTG TTT      391
Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val His Asp Val Leu Phe
  85                               90                               95

GGA GAT GTC TGG CTC TGT AGT GGG CAG AGT AAC ATG CAG ATG ACC GCG      439
Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn Met Gln Met Thr Ala
 100                               105                               110                               115

CGG GTC TTC AGA TGG CGT CAT GTG KTG GGG CTT TTA                        475
Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu Leu
                               120                               125

```

(2) INFORMATION FOR SEQ ID NO: 139:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 82..357
id AA075901
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..298
id H25630
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 3..298
id H43485
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..285
id H80718
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 28..303
id AA044211
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

seq LLTIVGLILPTRG/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

ACCTCTCTCC ACGAGGCTGC CGGCTTAGGA CCCCCAGCTC CGAC ATG TCG CCC TCT      56
                               Met Ser Pro Ser
                               -20

GGT CGC CTG TGT CTT CTC ACC ATC GTT GGC CTG ATT CTC CCC ACC AGA      104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
-15                               -10                               -5

GGA CAG ACG TTG AAA GAT ACC ACG TCC AGT TCT TCA GCA GAC TCA ACT      152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr
      1                               5                               10                               15

ATC ATG GAC ATT CAG GTC CCG ACA CGA GCC CCA GAT GCA GTC TAC ACA      200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
                               20                               25                               30

GAA CTC CAG CCC ACC TCT CCA ACC CCA ACC TGG CCT GCT GAT GAA ACA      248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
                               35                               40                               45

CCA CAA CCC CAG ACC CAG ACC CAG CAA CTG GAA GGA ACG GAT GGG CCT      296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
      50                               55                               60

CTA GTG ACA GAT CCA GAG ACA CCA CGG      323
Leu Val Thr Asp Pro Glu Thr Pro Arg
      65                               70

```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 43..330
id W31335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..63

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..42
id W31335
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..352
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 2..326
id AA094921
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 23..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..323
id AA055130
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..183
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 60..181
id R16450
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..245
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 179..244
id R16450
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 18..61
id R16450
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..183
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 75..192
id H94808
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 197..254
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 208..265
 id H94808
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 13..153
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.3
 seq LALSSLLSLLLFA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ARGCGCTGAC GC ATG CGC ATA GCT AAC CGC ACC CGG TTC AGC TTG CCT TTC      51
      Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe
              -45                      -40                      -35

TTG GCC AGA GGC GCC GGT TGG ACT CAC GGG CGG GGC ATG ATG GTG GTG      99
Leu Ala Arg Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val
              -30                      -25                      -20

GGT ACG GGC ACC TCG CTG GCG CTC TCC TCC CTC CTG TCC CTG CTG CTC     147
Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu
              -15                      -10                      -5

TTT GCT GGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC ACC GAG TGG     195
Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp
              1                      5                      10

CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC TTC GTG TTC TCG     243
Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser
              15                      20                      25                      30

CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT GGC AAA GGA TTC     291
Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe
              35                      40                      45

CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC CTG TTG GCT CTC     339
Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu
              50                      55                      60

TTT GCA TCT GGC CCG                                             354
Phe Ala Ser Gly Pro
              65
  
```

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..209
id R54127
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 221..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 199..295
id R54127
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 10..303
id R60167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..205
id H29628
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 211..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 185..291
id H29628
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 85..289
id N40052
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 28..116
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..89
id N40052
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..230
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 10..216
id R34889
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 221..279
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 206..264
id R34889
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..166
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.3
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

ATCTGTGCTG CTGGCCTGGG GTTGTGGTTG AGGCCGTGTC TCCGCTCCTG TGCCCGGGAA	60
G ATG GTG CTA GGT GGT TGC CCG GTT AGT TAC TTA CTT CTG TGC GGC CAG	109
Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln	
-35 -30 -25 -20	
GCG GCT TTG CTG CTG GGG AAT TTA CTT CTG CTG CAT TGT GTG TCT CGG	157
Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg	
-15 -10 -5	
AGC CAC TCG CAA AAT GCG ACC GCT GAG CCT GAG CTC ACA TCC GCT GGC	205
Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly	
1 5 10	
GCC GCC CAG CCG GAG GGC CCC GGG GGT GCT GCG AGC TGG GAA TAT GGC	253
Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly	
15 20 25	
GAC CCC CAC TCT CCG GTC ATC CTC TGM TCT TAC CTA CCT GAT GAA TTT	301
Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe	
30 35 40 45	
ATA GAA TGT GAA GAC CGG	319
Ile Glu Cys Glu Asp Arg	
50	

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 263..319
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 318..365
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 232..268
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..291
id W52428
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 361..453
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 298..390
 id W52428
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 79..237
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.1
 seq IYALFLLVGVCVA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

AAGTAAATAA TCTCGGAAAG GCGAGAAAGA AGCTGTCTCC ATCTTGTCTG TATCCGCTGC      60
TCTTGTGACG TTGTGGAG ATG GGG AGC GTC CTG GGG CTG TGC TCC ATG GCG      111
          Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala
                      -50                      -45

AGC TGG ATA CCA TGT TTG TGT GGA AGT GCC CCG TGT TTG CTA TGC CGA      159
Ser Trp Ile Pro Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg
          -40                      -35                      -30

TGC TGT CCT AGT GGA AAC AAC TCC ACT GTA ACT AGA TTG ATC TAT GCA      207
Cys Cys Pro Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala
          -25                      -20                      -15

CTT TTC TTG CTT GTT GGA GTA TGT GTA GCN TGT GTA ATG TTG ATA CCA      255
Leu Phe Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro
          -10                      -5                      1                      5

GGA ATG GAA GAA CAA CTG AAT AAG ATT CCT GGA TTT TGT GAG AAT GAG      303
Gly Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
          10                      15                      20

AAA GGT GTT GTC CCT TGT AAC ATT TTG GTT GGC TAT AAA GCT GTA TAT      351
Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr
          25                      30                      35

CGT TTG TGC TTT GGT TTG GCT ATG HTC TAT CTT CTT CTC TCT TTA CTA      399
Arg Leu Cys Phe Gly Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu
          40                      45                      50

ATG ATC AAA GTG AAG AGT AGC AGT GAT CCT AGA GCT GCA GTG CAC AAT      447
Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn
          55                      60                      65                      70

GGA TTT      453
Gly Phe

```

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 61..243
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 41..223
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 236..272
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 217..253
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 314..349
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 298..333
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 268..300
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 250..282
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 268..434
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 211..377
 id H30432
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 147..218
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 88..159
id H30432
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 209..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 151..213
id H30432
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 250..434
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 71..255
id H08060
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 35..87
id H08060
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 449..478
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 268..297
id H08060
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 61..149
id AA088762
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 201..253
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 185..237
id AA088762
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 19..64
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..46
 id AA088762
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 251..284
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 236..269
 id AA088762
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 126..252
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 102..228
 id HSCOWG121
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 61..127
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 36..102
 id HSCOWG121
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 31..201
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8
 seq IVRLVAFCPFASS/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AATNGCGAGC	NGAACCCGGC	AGCTGGCGCC	ATG GTG CTG TTG CAC GTG CTG TTT	54
			Met Val Leu Leu His Val Leu Phe	
			-55 -50	
GAG CAC GCG GTC GGC TAC GCG CTG CTG GCG CTG AAG GAA GTG GAG GAG	102			
Glu His Ala Val Gly Tyr Ala Leu Leu Ala Leu Lys Glu Val Glu Glu				
-45 -40 -35				
ATC AGT CTG CTG CAG CCG CAG GTG GAG GAG TCC GTG CTC AAC CTG GGC	150			
Ile Ser Leu Leu Gln Pro Gln Val Glu Glu Ser Val Leu Asn Leu Gly				
-30 -25 -20				
AAA TTC CAC AGC ATC GTT CGT CTG GTG GCC TTT TGT CCC TTT GCC TCA	198			
Lys Phe His Ser Ile Val Arg Leu Val Ala Phe Cys Pro Phe Ala Ser				
-15 -10 -5				
TCC CAG GTT GCC TTG GAA AAT GCC AAC GCC GTG TCT GAA GGG GTT GTT	246			

Ser	Gln	Val	Ala	Leu	Glu	Asn	Ala	Asn	Ala	Val	Ser	Glu	Gly	Val	Val	
1					5					10					15	
CAT	GAG	GAC	CTC	CGC	CTG	CTC	TTG	GAG	ACC	CAC	CTG	CCG	TCC	AAA	AAG	294
His	Glu	Asp	Leu	Arg	Leu	Leu	Leu	Glu	Thr	His	Leu	Pro	Ser	Lys	Lys	
			20					25						30		
AAG	AAA	GTA	CTC	TTG	GGA	GTT	GGG	GAT	CCC	AAG	ATT	GGT	GCC	GCA	ATA	342
Lys	Lys	Val	Leu	Leu	Gly	Val	Gly	Asp	Pro	Lys	Ile	Gly	Ala	Ala	Ile	
		35					40						45			
CAG	GAG	GAG	TTA	GGG	TAC	AAC	TGC	CAG	ACT	GGA	GGA	GTC	ATA	GCT	GAG	390
Gln	Glu	Glu	Leu	Gly	Tyr	Asn	Cys	Gln	Thr	Gly	Gly	Val	Ile	Ala	Glu	
		50				55						60				
ATC	CTG	CGA	RGA	GTT	CGT	CTG	CAC	TTC	CAC	AAT	CTG	GTG	AAA	GGG	TCT	438
Ile	Leu	Arg	Xaa	Val	Arg	Leu	His	Phe	His	Asn	Leu	Val	Lys	Gly	Ser	
		65				70					75					
GAC	CGA	TGT	GKT	CAG	CTT	GTA	AAG	CAC	AGC	TGG	GGC	TGG	GAC	ACA	GCT	486
Asp	Arg	Cys	Xaa	Gln	Leu	Val	Lys	His	Ser	Trp	Gly	Trp	Asp	Thr	Ala	
	80				85					90					95	
ATT	CCC	ATG														495
Ile	Pro	Met														

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 20..263
id H52756
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..186
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 10..195
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 182..272
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..255
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..180
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 167..257
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..228
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 29..243
id T73900
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 83..223
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
GAAGAGGCCG CTCTTCCTGG GGTGTTTCT CCGTGTGACG TGTGGCCTTT GAGATCAACT   60
CTCCTGTACC AGCGTAGGCC GC ATG AGT GGG GGG CGG GCT CCC GCG GTC CTG   112
               Met Ser Gly Gly Arg Ala Pro Ala Val Leu
               -45                               -40
CTC GGC GGA GTG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG   160
```

```

Leu Gly Gly Val Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
      -35                -30                -25

CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG    208
Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu
      -20                -15                -10

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT    256
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp
      -5                1                5                10

TCC GGC ATC GGG                                268
Ser Gly Ile Gly
      15

```

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..177
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..164
id T09311
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 54..131
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ATGAGATCCC GGCCTCAGGG TGGACGCACT GGTTCCTGCAC TGAGGCCCTC GTC ATG    56
                                   Met

GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT    104
Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe
-25                -20                -15                -10

ATC CTC TTC CTG ACT CGC AGC CGG GGC CGG GCG GCA TCA GCC GGC CAA    152
Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln
      -5                1                5

```

GAG CCA CTG CAC AAT GAG GAG CCG GGG
Glu Pro Leu His Asn Glu Glu Pro Gly
10 15

179

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..432
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 300..403
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 70..161
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 185..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 153..246
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..77
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 275..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 244..295
id AA182502
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..128
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..88
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 275..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 240..321
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 206..278
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 170..242
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..412
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 314..378
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 141..194
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 103..156
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..273
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 37..207
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 323..432

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 259..368
 id W52153
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 272..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 207..261
 id W52153
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 66..109
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 1..44
 id W52153
 est

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 38..181
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ACGACGCCGG CGAGCAGTGG CCGTKACGGC CGAAAAG ATG GCG GTC TTG GCA CCT	55
Met Ala Val Leu Ala Pro	
-45	
CTA ATT GCT CTC GTG TAT TCG GTG CCG CGA CTT TCA CGA TGG CTC GCC	103
Leu Ile Ala Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala	
-40 -35 -30	
CAA CCT TAC TAC CTT CTG TCG GCC CTG CTC TCT GCT GCC TTC CTA CTC	151
Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu	
-25 -20 -15	
GTG AGG AAA CTG CCG CCG CTC TGC CAC GGT CTG CCC ACC CAA MGC GAA	199
Val Arg Lys Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Xaa Glu	
-10 -5 1 5	
GAC GGT AAC CCG TGT GAC TTT GAC TGG AGA GAA GTG GAG ATC CTG ATG	247
Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met	
10 15 20	
TTT CTC AGT GCC ATT GTG ATG ATG AAG AAC CGC AGA TCC ATC ACT GTG	295
Phe Leu Ser Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val	
25 30 35	
GAG CAA CAT ATA GGC AAC ATT TTC ATG TTT AGT AAA GTG GCC AAC ACA	343
Glu Gln His Ile Gly Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr	
40 45 50	

ATT CTT TTC TTC CGC TTG GAT ATT CGC ATG GGC CTA CTT TAC ATC ACA 391
Ile Leu Phe Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr
55 60 65 70

CTC TGC ATA GTG TTC CTG ATG ACG TGC AAA CCC CCC CTT 430
Leu Cys Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu
75 80

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..88
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 309..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 240..321
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 240..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 170..242
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 382..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 314..378
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 175..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 103..156
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 137..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 37..207
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..453
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 259..355
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 306..360
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 207..261
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..44
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 48..300
id H15999
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..42
id H15999

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 9..215
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

AAGTCGTT ATG GTG GGG GAG GCG GGG CGA GAC CTA CGA CGC CGG CGA SCW      50
  Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa
                    -65                      -60

KTG GCC GTT ACG GCC GDD AAG ATG GCG GTC TTG GCA CCT CTA ATT GCT      98
Xaa Ala Val Thr Ala Xaa Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-55                    -50                      -45                      -40

CTC GTG TAT TCG GTG CCG CGA CTT TCA CGA TGG CTC GCC CAA CCT TAC      146
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
                    -35                      -30                      -25

TAC CTT CTG TCG GCC CTG CTC TCT GCT GCC TTC CTA CTC GTG AGG AAA      194
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
                    -20                      -15                      -10

CTG CCG CCG CTC TGC CAC GGT CTG CCC ACC CAA CGC GAA GAC GGT AAC      242
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn
                    -5                      1                      5

CCG TGT GAC TTT GAC TGG AGA GAA GTG GAG ATC CTG ATG TTT CTC AGT      290
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
10                    15                      20                      25

GCC ATT GTG ATG ATG AAG AAC CGC AGA TCC ATC ACT GTG GAG CAA CAT      338
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His
                    30                      35                      40

ATA GCC AAC ATT TTC ATG TTT AGT AAA GTG GCC AAC ACA ATT CTT TTC      386
Ile Ala Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe
                    45                      50                      55

TTC CGC TTG GAT ATT CGC ATG GGC CTA CTT TAC ATC ACA CTC TGC ATA      434
Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile
                    60                      65                      70

GTG TTC CTG ATG ACG TGC      452
Val Phe Leu Met Thr Cys
                    75

```

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 178..304
id W69812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..124
id W69812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 359..423
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 302..366
id W69812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..177
id W69812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..361
id T09075
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..308
id W45253
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 386..438
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 309..361
 id W45253
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 18..417
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 1..400
 id AA105440
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 2..288
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 9..295
 id H42261
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 21..164
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq LLMLLLFLSELQY/YL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

ACCCTTTCCG GMMGGTCCCC ATG GAG GCG CTG GGG AAG CTG AAG CAG TTC GAT   53
      Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp
                        -45                      -40

GCC TAC CCC AAG ACT TTG GAG GAC TTC CGG GTC AAG ACC TGC GGG GGC   101
Ala Tyr Pro Lys Thr Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly
      -35                      -30                      -25

GCC ACC GTG ACC ATT GTC AGT GGC CTT CTC ATG CTG CTA CTG TTC CTG   149
Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu
      -20                      -15                      -10

TCC GAG CTG CAG TAT TAC CTC ACC ACG GAG GTG CAT CCT GAG CTC TAC   197
Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr
      -5                        1                        5                        10

GTG GAC AAG TCG CGG GGA GAT AAA CTG AAG ATC AAC ATC GAT GTA CTT   245
Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu
      15                        20                        25

TTT CCG CAC ATG CCT TGT GCC TAT CTG AGT ATT GAT GCC ATG GAT GTG   293
Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val
      30                        35                        40

```

```
GCC GGA GAA CAG CAG CTG GAT GTG GAA CAC AAC CTG TTC AAG CAA CGA      341
Ala Gly Glu Gln Gln Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg
   45                      50                      55

CTA GAT AAA GAT GGC ATC CCC GTG AGC TCA GAG GCT GAG CGG CAT GAG      389
Leu Asp Lys Asp Gly Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu
   60                      65                      70                      75

CTT GGG AAA GTC GAG GTG ACG GTG TTT GAC CCT GAC TCC CTG GAC CCG      437
Leu Gly Lys Val Glu Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro
   80                      85                      90
```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 70..161
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 300..392
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..253
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 153..246
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..84
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..77

id AA182502
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 250..301
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 244..295
id AA182502
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 78..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 37..207
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 298..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 259..357
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 247..301
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 207..261
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..84
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..44
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 409..445
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 370..406
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..103
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..88
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 250..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 240..321
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..253
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 170..242
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 323..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 314..378
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 116..169
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 103..156
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 409..446
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 444..481
id W57342
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

ACGGCCGAAA AG ATG GCG GTC TTG GCA CCT CTA ATT GCT CTC GTG TAT TCG 51

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser
 -45 -40

GTG CCG CGA CTT TCA CGA TGG CTC GCC CAA CCT TAC TAC CTT CTG TCG 99
 Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser
 -35 -30 -25 -20

GCC CTG CTC TCT GCT GCC TTC CTA CTC GTG AGG AAA CTG CCG CCG CTC 147
 Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu
 -15 -10 -5

TGC CAC GGT CTG CCC ACC CAA CGC GAA GAC GGT AAC CNN TGT GAC TTT 195
 Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe
 1 5 10

GAC TGG AGA GAA GTG GAG ATC CTG ATG TTT CTC AGT GCC ATT GTG ATG 243
 Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met
 15 20 25

ATG AAG AAC CGC AGA TCC ATC ACT GTG GAG CAA CAT ATA GGC AAC ATT 291
 Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile
 30 35 40 45

TTC ATG TTT AGT AAA GTG GCC AAC ACA ATT CTT TTC TTC CGC TTG GAT 339
 Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp
 50 55 60

ATT CGC ATG GGC CTA CTT TRC ATC ACA CTC TGC ATA GTG TTC CTG ATG 387
 Ile Arg Met Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met
 65 70 75

ACG TGC AAA CCC CCC CTA TAT ATG GGC CCT GAG TAT ATC AVG TAC TTC 435
 Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe
 80 85 90

AAT GAT AAA 444
 Asn Asp Lys
 95

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
 region 1..272

id C18312
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 259..385
id C18312
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 87..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 59..265
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 252..339
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 22..68
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 92..252
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 239..314
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..94
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 25..55
id T78951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..132
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 62..92
id T78951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 133..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 144..305
id W69247
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 280..332
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 292..344
id W69247
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 49..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 62..108
id W69247
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 97..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 69..280
id H75891
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..69
id H75891
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 306..335
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 280..309
 id H75891
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 55..111
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.4
 seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

AGCCTCCCGA TTGACTGGCC TGCTTGGCAA BGCAAGTAGC GGCGGCGCTT CAAG ATG      57
                                     Met

CGC TGC CTG ACC ACG CCT ATG CTG CTG CGG GCC CTG GCC CAG GCT GCA      105
Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala Ala
      -15                      -10                      -5

CGT GCA GGA CCT CCT GGT GGC CGG AGC CTC CAC AGC AGT GCA GTG GCA      153
Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val Ala
      1                      5                      10

GCC ACC TAC AAG TAT GTG AAC ATG CAG GAT CCC GAG ATG GAC ATG AAG      201
Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met Lys
      15                      20                      25                      30

TCA GTG ACT GAC CGG GCA GCC CGC ACC CTG CTG TGG ACT GAG CTC TTC      249
Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu Phe
      35                      40                      45

CGA GGC CTG GGC ATG ACC CTG AGC TAC CTG TTC CGG GAA CCG GCC ACC      297
Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala Thr
      50                      55                      60

ATC AAC TAC CCG TTC GAG AAG GGC CCG CTG AGC CCT CGC TTC CGT GGG      345
Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg Gly
      65                      70                      75

GAG CAT GCG CTG CGC CGG TAC CCA TCC GGG GAG GAG CGT TGC ATT GCC      393
Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile Ala
      80                      85                      90

TGC AAG CTC TGC      405
Cys Lys Leu Cys
      95
  
```

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 13..272
id C18312
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 259..425
id C18312
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 59..265
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 22..63
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 92..252
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 239..314
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 62..92
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 25..55
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..277
id C16677
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 69..280
id H75891
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 8..69
id H75891
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 280..309
id H75891
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 23..79
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

AAAGTAGCGG CGGCGCTTCA AG ATG CGC TGC CTG ACC ACG CCT ATG CTG CTG	52
Met Arg Cys Leu Thr Thr Pro Met Leu Leu	
-15 -10	
CGG GCC CTG GCC CAG GCT GCA CGT GCA GGA CCT CCT GGT GGC CGG AGC	100
Arg Ala Leu Ala Gln Ala Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser	
-5 1 5	
CTC CAC AGC AGT GCA GTG GCA GCC ACC TAC AAG TAT GTG AAC ATG CAG	148
Leu His Ser Ser Ala Val Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln	
10 15 20	
GAT CCC GAG ATG GAC ATG AAG TCA GTG ACT GAC CGG GCA GCC CGC ACC	196
Asp Pro Glu Met Asp Met Lys Ser Val Thr Asp Arg Ala Ala Arg Thr	
25 30 35	
CTG CTG TGG ACT GAG CTC TTC CGA GGC CTG GGC ATG ACC CTG AGC TAC	244
Leu Leu Trp Thr Glu Leu Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr	
40 45 50 55	
CTG TTC CGG GAA CCG NCC ACC ATC AAC TAC CCG TTC GAG AAG GGC CCG	292
Leu Phe Arg Glu Pro Xaa Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro	
60 65 70	
CTG AGC CCT CGC TTC CGT GGG GAG CAT GCG CTG CGC CGG TAC CCA TCC	340
Leu Ser Pro Arg Phe Arg Gly Glu His Ala Leu Arg Arg Tyr Pro Ser	
75 80 85	
GGG GAG GAG CGT TGC ATT GCC TGC AAG CTC TGC GAG GCC ATC TGC CCC	388
Gly Glu Glu Arg Cys Ile Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro	
90 95 100	
GCC CAG GCC ATC ACC ATC GAG GCT GAG	415
Ala Gln Ala Ile Thr Ile Glu Ala Glu	
105 110	

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..349

id N40260
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 349..400
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 351..402
id N40260
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..400
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 22..369
id W37568
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 14..297
id AA135041
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 335..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 297..358
id AA135041
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 114..300
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 74..260
id W00732
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 302..386
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 263..347
id W00732
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..284
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 16..299
id W07706
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 285..323
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 301..339
id W07706
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..121
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq ILPLLFGCLGVFG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

GAAGTTGCTT GACTATGGTC TCTCCGGCTA CCAGGAAGAG TCTGCCGAAG TGAAGGCC      58

ATG GAC TTC ATC ACC TCC ACA GCC ATC CTG CCC CTG CTG TTC GGC TGC      106
Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
-20                               -15                               -10

CTG GGC GTC TTC GGC CTC TTC CGG CTG CTG CAG TGG GTG CGC GGG AAG      154
Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5                               1                               5                               10

GCC TAC CTG CGG AAT GCT GTG GTG GTG ATC ACA GGC GCC ACC TCA GGG      202
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15                               20                               25

CTG GGC AAA GAA TGT GCA AAA GTC TTC TAT GCT GCG GGT GCT AAA CTG      250
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30                               35                               40

GTG CTC TGT GGC CGG AAT GGT GGG GCC CTA GAA GAG CTC ATC AGA GAA      298
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45                               50                               55

CTC ACC GCT TCT CAT GCC ACC AAG GTG CAG ACA CAC AAG CCT TAC TTG      346
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60                               65                               70                               75

GTA CKN TTN GAC CTC ACA GAC TCT GGG GCC ATA GTT GCA GCA GCA GCT      394
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80                               85                               90

GAG ATC TGC AGT
Glu Ile Cys Ser
95

```

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 18..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..281
 id C17369
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 18..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..281
 id HUM522E11B
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 42..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..257
 id HUM503D01B
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 82..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 46..262
 id N30487
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 35..70
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..36
 id N30487
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 19..252

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..234
id C17067
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..248
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq LLLVTWVFPTT/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
AGTGTTCGCC GCTGGAGCCC GGGTCGAGAG GACGAGGTGC CGCTGCCTGG AGAATCCTCC    60
GCTGCCGTCG GCTCCCGGAG CCCAGCCCTT TCCTAACCCA ACCCAACCTA GCCCAGTCCC    120
AGCCGMCAGM GCCTGTCCCT RTCACGGACC CCAGCGTTAC C ATG CAT CCT GCC GTC    176
                                         Met His Pro Ala Val
                                         -25

TTC CTA TCC TTA CCC GAC CTC AGA TGC TCC CTT CTG CTC CTG GTA ACT    224
Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu Leu Leu Leu Val Thr
      -20                      -15                      -10

TGG GTT TTT ACT CCT GTA ACA ACT GAA ATA ACA AGT CTT GAT ACA GAG    272
Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr Ser Leu Asp Thr Glu
      -5                      1                      5

VGT ATA GAT GAA ATT TTA AAC AAT GCA TTG                                302
Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 76..259
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 97.3
region 1..184
id HSU72245
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 73..178
id W25639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 179..270
id W25639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 38..82
id W25639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 11..258
id R72515
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..228
id AA040016
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..223
id T84313
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..227
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 129..286
id H57207

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 225..259
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 285..319
id H57207
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
AAAGTGCTCA GCGCCCGGGG SACAGCAGGA CGTTTGGGGG CCTTCTTTCA GCAGGGGACA    60
GCGCGATTGG GGACA ATG GCG TCT CTT GGC CAC ATC TTG GTT TTC TGT GTG    111
      Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val
      -20                      -15                      -10

GGT CTC CTC ACC ATG GCC AAG GCA GAA AGT CCA AAG GAA CAC GAC CCG    159
Gly Leu Leu Thr Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro
      -5                      1                      5

TTC ACT TAC GAC TAC CAG TCC CTG CAG ATC GGA GGC CTC GTC ATC GCC    207
Phe Thr Tyr Asp Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala
      10                      15                      20

GGG ATC CTC TTC ATC CTG GGC ATC CTC ATC GTG CTG AGC AGA AGA TGC    255
Gly Ile Leu Phe Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys
      25                      30                      35                      40

CGG TTT CGG    264
Arg Phe Arg
```

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..444

(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 91.9
region 164..604
id RNGP55
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..444
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 90.6
region 567..901
id RNGP56
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..444
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 91.4
region 1..439
id D50463
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 205..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 300..393
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 120..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 214..299
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 95..156
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 56..119
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 149..212
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 297..340
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 393..436
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..339
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..321
id R14826
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 345..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 330..362
id R14826
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..444
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 133..408
id W75505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..138
id W75505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..246
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 165..352
id AA206770
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 284..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 393..460
id AA206770
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 1..69
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 105..173
 id AA206770
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 243..286
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 351..394
 id AA206770
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 169..415
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 133..379
 id W64115
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 34..171
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 1..138
 id W64115
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..98
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.3
 seq ALSLLLVSGLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATTCGCTGTT GGGTCTTCTG CTAGGGAGG ATG TCG GGT TCG TCG CTG CCC AGC	53
Met Ser Gly Ser Ser Leu Pro Ser	
-20	
GCC CTG GCC CTC TCG CTG TTG CTG GTC TCT GGC TCC CTC CTC CCA GGG	101
Ala Leu Ala Leu Ser Leu Leu Val Ser Gly Ser Leu Leu Pro Gly	
-15 -10 -5 1	
CCA GGC GCC GGT CAG AAC GAG CCA AGG ATT GTC ACC AGT GAA GAG GTC	149
Pro Gly Ala Ala Gln Asn Glu Pro Arg Ile Val Thr Ser Glu Glu Val	
5 10 15	
ATT ATT CGA GAC AGC CCT GTT CTC CCT GTC ACC CTG CAG TGT AAC CTC	197
Ile Ile Arg Asp Ser Pro Val Leu Pro Val Thr Leu Gln Cys Asn Leu	

20	25	30	
ACC TCC AGC TCT CAC ACC CTT ACA TAC AGC TAC TGG ACA AAG AAT GGG			245
Thr Ser Ser Ser His Thr Leu Thr Tyr Ser Tyr Trp Thr Lys Asn Gly			
35	40	45	
GTG GAA CTG AGT GCC ACT CGT AAG AAT GCC AGC AAC ATG GAG TAC AGG			293
Val Glu Leu Ser Ala Thr Arg Lys Asn Ala Ser Asn Met Glu Tyr Arg			
50	55	60	65
ATC AAT AAG CCG AGA GCT GAG GAT TCA GGC GAA TAC CAC TGC GTA TAT			341
Ile Asn Lys Pro Arg Ala Glu Asp Ser Gly Glu Tyr His Cys Val Tyr			
70	75	80	
CAC TTT GTC AGC GCT CCT AAA GCA AAC GCC ACC ATT GAA GTG AAA GCC			389
His Phe Val Ser Ala Pro Lys Ala Asn Ala Thr Ile Glu Val Lys Ala			
85	90	95	
GCT CCT GAC ATC ACT GGC CAT AAA CGG AGT DAG AAC AAG AAT GAA GGG			437
Ala Pro Asp Ile Thr Gly His Lys Arg Ser Xaa Asn Lys Asn Glu Gly			
100	105	110	
CAG GAT			443
Gln Asp			
115			

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..130
id AA056148
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 369..480
id AA056148
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..251
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 261..372
id AA056148
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 227..313
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 24..94
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 216..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 304..359
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 294..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 384..432
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..292
id HUM149F06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 150..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..331
id AA187561
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 140..423
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 77..360
 id W51338
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..244
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq IMLLSLAAFSVIS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

AGTCTGTCGG ASTCTGTCCT CGGAGCAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC    60
CGGATTATTC TATTTCCCCT CCCTCTCTSC CGCCCCGTAT CTCTTTTCAC CCTTCTCCCA    120
CCCTCGCTCG CGTRSC ATG GCG GTG CAC GAT CTG ATT TTC TGG AGA GAT GTG    172
      Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val
      -35                      -30                      -25

AAG AAG ACT GGG TTT GTC TTT GGC ACC ACG CTG ATC ATG CTG CTT TCC    220
Lys Lys Thr Gly Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser
      -20                      -15                      -10

CTG GCA GCT TTC AGT GTC ATC AGT GTG GTT TCT TAC CTC ATC CTG GCT    268
Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala
      -5                      1                      5

CTT CTC TCT GTC ACC ATC AGC TTC AGG ATC TAC AAG TCC GTC ATC CAA    316
Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Ile Gln
      10                      15                      20

GCT GTA CAG AAG TCA GAA GAA GGC CAT CCA TTC AAA GCC TAC CTG GAC    364
Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp
      25                      30                      35                      40

GTA GAC ATT ACT CTG TCC TCA GAA GCT TTC CAT AAT TAC ATG AAT GCT    412
Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala
      45                      50                      55

GCS ATG GTG CAC    424
Ala Met Val His
      60

```

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 194..260

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 171..237
id AA213022
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 35..130

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.1
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```

CTGGCACCTC TTCCGTCGGC TGAATTGCGG CCGT ATG CRC GGC TCT GTG GAG TGC      55
                               Met Xaa Gly Ser Val Glu Cys
                               -30

ACC TRG GGT TGG GGG CAC TGT GCC CCC AGC CCC CTG CTC CTT TGG ACT      103
Thr Xaa Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr
-25                -20                -15                -10

CTA CTT CTG TTT GCA GCC CCA TTT GGC CTG CTG GGG GAG AAG ACC CGC      151
Leu Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg
          -5                1                5

CAG GTG TCT CTG GAG GTC ATC CCT AAC TGG CTG GGC CCC CTG CAG AAC      199
Gln Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn
          10                15                20

CTG CTT CAT ATA CGG GCA GTG GGC ACC AAT TCC ACA CTG CAC TAT GTG      247
Leu Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val
          25                30                35

TGG AGC AGC CTG GGG CCT CTG GCA GTG GTA ATG GTG GCC ACC AAC ACC      295
Trp Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr
          40                45                50                55

CCC CCC GGG                                                              304
Pro Pro Gly

```

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 47..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 30..314
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 330..429

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 314..413
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 47..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 30..314
id AA161042
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 338..422

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 323..407
id AA161042
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 23..335

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..313
id H64488
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 129..354
id AA088770
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 32..121
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 17..106
 id AA088770
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 116..317
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 134..335
 id AA146605
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 317..378
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 336..397
 id AA146605
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..223
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```

AAGTGGTGTG TGAGAGCCAG GCGTCCCTCT GCCTGCCAC TCAGTGGCAA CACCCGGGAG   60
CTGTTTGTGC CTTGTGGAG CCTCAGCAGT TCCCTCTTTC AGAACTCACT GCCAAGAGCC   120
CTGAACAGGA GCCACC ATG CAG TGC TTC AGC TTC ATT AAG ACC ATG ATG ATC   172
      Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile
                        -25                      -20

CTC TTC AAT TTG CTC ATC TTT CTG TGT GGT GCA GCC CTG TTG GCA GTG   220
Leu Phe Asn Leu Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val
      -15                      -10                      -5

GGC ATC TGG GTG TCA ATC GAT GGG GCA TCC TTT CTG AAG ATC TTC GGG   268
Gly Ile Trp Val Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly
      1                      5                      10                      15

CCA CTG TCG TCC AGT GCC ATG CAG TTT GTC AAC GTG GGC TAC TTC CTC   316
Pro Leu Ser Ser Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu
                        20                      25                      30

ATC GCA GCC GGC GTT GTG GTC TTT GCT CTT GGT TTC CTG GGC TGC WMT   364
Ile Ala Ala Gly Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa
      35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 159:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AAGAATTGGCG GCGGT ATG CGC GGC TCT GTG GAG TGC ACC TGG GGT TSG GGG 51
 Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly
 -30 -25

CAC TGT GCC CCC AGC CCC CTG CTC CTT TGG ACT CTA CTT CTG TTT GCA 99
 His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala
 -20 -15 -10 -5

WO 99/06548

211

PCT/IB98/01222

GCC CCA TTT GGC CTG CTG GGG GAG AAG ACC CAC CAG GTG TCT CTG GAG	147
Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu	
1 5 10	
GTC ATC CCT AAC TGG CTG GGC CCC CTG CAG AAC CTG CTT CAT ATA CGG	195
Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg	
15 20 25	
BCA GTG GGC ACC AAT TCC ACA CTG CAC TAT GTG TGG AGC AGC CTG GGG	243
Xaa Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly	
30 35 40	
CCT CTG GCA GTG GTA ATG GTG GCC ACC AAC ACC CCC CAC AGC ACC CTG	291
Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu	
45 50 55 60	
AGC GTC AAC TGG AGC CTC CTG CTA TCC CCT GAG CCC GAT GGG GGC CTG	339
Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu	
65 70 75	
ATG GTG CTC CCT AAG GAC AGC ATT CAG TTT TCT TCT	375
Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser	
80 85	

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 163..233
id AA113990
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 46..103
id AA113990
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..44

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..50
id AA113990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 113..142
id AA113990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 71..202
id R11825
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..68
id R11825
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 83..205
id H08475
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..72
id H08475
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 175..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 142..201
id C14102
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..103
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 25..68
id C14102
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 136..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..99
id N87606
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..82
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7
seq LRLKLAATSASA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
ACCCTTGGGT CCTTGATCCT GAGCTGACCG GGTAGCC ATG GCC TTG CGG CTC CTG      55
                                   Met Ala Leu Arg Leu Leu
                                   -15                               -10

AAG CTG GCA GCG ACG TCC GCG TCC GCC CGG GTC CTG GCG GCG GGC GCC      103
Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg Val Val Ala Ala Gly Ala
               -5                               1                               5

CAG CGC GTG AGA GGA ATT CAT AGC AGT GTG CAG TGC AAG CTG CGC TAT      151
Gln Arg Val Arg Gly Ile His Ser Ser Val Gln Cys Lys Leu Arg Tyr
               10                               15                               20

GGA ATG TGG CAT TTC CTA CTT GGG GAT AAA GCA AGC AAA AGA CTG ACA      199
Gly Met Trp His Phe Leu Leu Gly Asp Lys Ala Ser Lys Arg Leu Thr
               25                               30                               35

GAA CGC AGC AGA GTG ATA ACT GTA GAT GGC AAT ATG                      235
Glu Arg Ser Arg Val Ile Thr Val Asp Gly Asn Met
               40                               45                               50
```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..399
id AA233701
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 7..50
id AA233701
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 148..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 106..367
id N39913
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..108
id N39913
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 42..169
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 39..166
id HUM527C01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..284
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 165..280
id HUM527C01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..42
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100

region 1..38
id HUM527C01B
.est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..118
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..107
id AA280711
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..256
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

CTCTGTGGAT TCTGGCCAGG CCGGGTTCGG CGGTTGCTGT GAGAGCGGGC TTCCCAACAC      60
C ATG CCG TCC GCC TTC TCT GTC AGC TCT TTC CCC GTC AGC ATC CCA GCC      109
  Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
  -65                -60                -55                -50

GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG CTC ATG GGG CTG GCC      157
Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
      -45                -40                -35

ACC TTC CAC GCG CTC TGC GTG CTC CTC ACC TGC TTG TCC TCC CGA AGC      205
Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
      -30                -25                -20

TAC AGA CTA CAG ATC GGG CAC TTT CTG TGT CTA GTC ATC TTA GTC TAC      253
Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
      -15                -10                -5

TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG AAC TGG AGA TTA TTT      301
Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
      1                5                10                15

TCG AAA TAC CAG TAT TTC GAC TCC AGG GGG ATG TTC ATT TCT ATA GTA      349
Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
      20                25                30

TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC ATT GTG GTT ATG TGG      397
Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
      35                40                45

GTA TGG AAG ACT      409
Val Trp Lys Thr
      50

```

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 514 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 220..364
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 192..336
 id T53942
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 88..223
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 59..194
 id T53942
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 31..88
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..58
 id T53942
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 371..409
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 345..383
 id T53942
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 32..349
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 47..364
 id R55646
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 2..35
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 18..51
id R55646
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 47..238
id H21573
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 220..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 236..341
id H21573
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..35
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 18..51
id H21573
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..296
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 2..254
id W47454
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 265..304
id W47454
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 395..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 360..391
id W47454
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 39..223
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 36..220
 id T71932
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 220..272
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 218..270
 id T71932
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 4..37
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 2..35
 id T71932
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 26..487
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

AAHCAGACCT CCTCTGGCT TCGAG ATG GCT TTG CCA CAC CAA GAG CCC AAA	52
Met Ala Leu Pro His Gln Glu Pro Lys	
-150	
CCT GGA GAC CTG ATT GAG ATT TTC CGC CTT GGC TAT GAG CAC TGG GCC	100
Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala	
-145 -140 -135 -130	
CTG TAT ATA BGA GAT GGC TAC GTG ATC CAT CTG GCT CCT CCA AGT GAG	148
Leu Tyr Ile Xaa Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu	
-125 -120 -115	
TAC CCC GGG GCT GGC TCC TCC AGT GTC TTC TCA GTC CTG AGC AAC AGT	196
Tyr Pro Gly Ala Gly Ser Ser Ser Val Phe Ser Val Leu Ser Asn Ser	
-110 -105 -100	
GCA GAG GTG AAA CGG GAG CGC CTG GAA GAT GTG GTG GGA GGC TGT TGC	244
Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys	
-95 -90 -85	
TAT CGG GTC AAC AAC AGC TTG GAC CAT GAG TAC CAA CCA CGG CCC GTG	292
Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val	
-80 -75 -70	
GAG GTG ATC ATC AGT TCT GCG AAG GAG ATG GTT GGT CAG AAG ATG AAG	340
Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys	

-65	-60	-55	-50	
TAC AGT ATT GTG AGC AGG AAC TGT GAG CAC TTT GTC ACC CAG CTG AGA				388
Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg				
	-45	-40	-35	
TAT GGC AAG TCC CGC TGT AAA CAG GTG GAA AAG GCC AAG GTT GAA GTC				436
Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val				
	-30	-25	-20	
GGT GTG GCC ACG GCG CTT GGA ATC CTG GTT GTT GCT GGA TGC TCT TTT				484
Gly Val Ala Thr Ala Leu Gly Ile Leu Val Val Ala Gly Cys Ser Phe				
	-15	-10	-5	
GCG ATT AGG AGA TAC CAA AAA AAA GCG ACC				514
Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr				
1	5			

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..119
id AA114211
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 143..225
id AA114211
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 30..113
id AA121286
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 214..287
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 177..250
 id AA121286
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 276..340
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 238..302
 id AA121286
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 35..64
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..30
 id AA121286
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 13..222
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LAFSLPALPLAEL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

AGAGTCGGGA AA ATG GCT GCG AGT ACC TCC ATG GTC CCG GTG GCT GTG ACG    51
      Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
      -70                      -65                      -60

GCG GCA GTG GCG CCT GTC CTG TCC ATA AAC AGC GAT TTC TCA GAT TTG    99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
      -55                      -50                      -45

CGG GAA ATT AAA AAG CAA CTG CTG CTT ATT GCG GGC CTT ACC CGG GAG    147
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
      -40                      -35                      -30

CGG GGC CTA CTA CAC AGT AGC AAA TGG TCG GCG GAG TTG GCT TTC TCT    195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
      -25                      -20                      -15                      -10

CTC CCT GCA TTG CCT CTG GCC GAG CTG CAA CCG CCT CCG CCT ATT ACA    243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
      -5                      1                      5

GAG GAA GAT GCC CAG GAT ATG GAT GCC TAT ACC CTG GCC AAG GCC TAC    291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
      10                      15                      20

```

TTT GAC GTT AAA GAG TAT GAT CGG GCA GCA CAT TTC CTG CAT GGC TGC	339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys	
25 30 35	
AAT GCA AGA WAA GCC TAT TTT CTG TAT ATG TAT TCC AGA TAT CTG TCT	387
Asn Ala Arg Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser	
40 45 50 55	

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 116..333
id H42954
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..111
id H42954
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 332..381
id H42954
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 275..404
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..224
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 94..194
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..89
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 191..288
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..111
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 197..294
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 144..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 120..199
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 307..349
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 281..323
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 372..408
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 346..382
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..224
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 65..165
id N79656
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 162..259
id N79656
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..60
id N79656
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 367..406
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 307..346
id N79656
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 86..291
id HUM424A03B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..81

id HUM424A03B
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 154..225
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq KMVHLLVLSGAWG/MQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```

AAAACCCACG AGGGGACGCG GCCGAGGAGG GTCGCTGTCC ACCCGGGGGC GTGGGAGTGA 60
GGTACCAGAT TCAGCCCAT TGGCCCCGAC GCCTCTGTTC TCGGAATCCG GGTGCTKGGC 120
GATTNRAGGT CCCGGTTCCT AACCGACTGC AAG ATG GAG GAA GGC GGG AAC CTA 174
Met Glu Glu Gly Gly Asn Leu
-20

GGA GGC CTG ATT AAG ATG GTC CAT CTA CTG GTC TTG TCA GGT GCC TGG 222
Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp
-15 -10 -5

GGC ATG CAA ATG TGG GTG ACC TTC GTC TCA GGC TTC CTG CTT TTC CGA 270
Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg
1 5 10 15

AGC CTT CCC CGA CAT ACC TTC GGA CTA GTG CAG AGC AAA CTC TTC CCC 318
Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro
20 25 30

TTC TAC TTC CAC ATC TCC ATG GGC TGT GCC TTC ATC AAY NTC TGC ATC 366
Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Xaa Cys Ile
35 40 45

TTG GCT TCA CAG CAT GCT TGG GCT CAG CTC ACA TTC TGG GAG GCC AGC 414
Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser
50 55 60

CAG CTT TAC CTG CTG TTC CTG 435
Gln Leu Tyr Leu Leu Phe Leu
65 70

```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 151..247
id W04736
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..33
id W04736
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 44..200
id HUM054D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..110
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 6..52
id HUM054D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 6..218
id HUM065G09B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..217
id HUM062A01B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..110
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 5..52

id HUM062A01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 10..135
id HUM048E08B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 179..276
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 124..221
id HUM048E08B
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 14..256
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq LLLASGTTLFCTS/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGTTCTACA GCT ATG GCC GGG CCA GCT GCA GCT TTC CGC CGC TTG GGC	49
Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly	
-80 -75 -70	
GCC TTG TCC GGA GCT GCG GCC TTA GGC TTC GCT TCC TAC GGG GCG CAC	97
Ala Leu Ser Gly Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His	
-65 -60 -55	
GGC GCC BAA TTC CCA GAT GCC TAC GGG AAG GAG CTG TTT GAC AAG GCC	145
Gly Ala Xaa Phe Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala	
-50 -45 -40	
AAC AAA CAC CAC TTC TTA CAC AGC CTG GCC CTG TTA GGG GTG CCC CAT	193
Asn Lys His His Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His	
-35 -30 -25	
TGC AGA AAG CCA CTC TGG GCT GGG TTA TTG CTA GCT TCC GGA ACG ACC	241
Cys Arg Lys Pro Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr	
-20 -15 -10	
TTA TTC TGC ACC AGC TTT TAC TAC CAG GCT CAG	274
Leu Phe Cys Thr Ser Phe Tyr Tyr Gln Ala Gln	
-5 1 5	

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..179
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..143
id H06750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..179
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 14..127
id R09748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..181
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..76
id AA025704
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq LLTLLPPLLYT/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

ACTCTTCCGG GTCGGCGCTC CTGCCTCCCT GCAGGGAGCT GCTT ATG GGA CAC CGC	56
Met Gly His Arg	
-20	
TTC CTG CGC GGC CTC TTA ACG CTG CTG CTG CCG CCG CCA CCC CTG TAT	104
Phe Leu Arg Gly Leu Leu Thr Leu Leu Pro Pro Pro Pro Leu Tyr	
-15 -10 -5	
ACC CGG CAC CGC ATG CTC GGT CCA GAG TCC GTC CCG CCC CCA AAA CGA	152
Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro Pro Pro Lys Arg	
1 5 10 15	
TCC CGC AGC AAA CTC ATG GCA CCG CCC CGG	182
Ser Arg Ser Lys Leu Met Ala Pro Pro Arg	

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 48..320
id AA081335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..80
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..49
id AA081335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 82..229
id H88204
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..98
id H88204
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..160

id W31695
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq ILFLLPsicssns/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

AACATTCACT ASRCCTTTTC CATTTGCTAA TAAGGCCCTG CCAGGCTGGG AGGGAATTGT 60
CCCTGCCTGC TTCTGGAGMA MAGAAGATAT TGACACCATC TACGGGCACC ATG GAA 116
                                         Met Glu
                                         -20

CTG CTT CAA GTG ACC ATT CTT TTT CTT CTG CCC AGT ATT TGC AGC AGT 164
Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser
-15 -10 -5

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TCA CTT GTT GTT ACT 212
Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr
1 5 10

ACA ACA AAW CCA TCT ATA ACA ACA CCA AAC ACA GAA TCA TTA CAG AAA 260
Thr Thr Xaa Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln Lys
15 20 25 30

AAT GTT GTC ACA CCA ACA ACT GGA ACA ACT CHT AAA GGA ACA ATC ACC 308
Asn Val Val Thr Pro Thr Thr Gly Thr Thr Xaa Lys Gly Thr Ile Thr
35 40 45

AAT GAA TTA CTT AAA ATG TCT CTG ATG TCA ACA GCT VCT TTT 350
Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Xaa Phe
50 55 60

```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..372
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 33..329

id H97426
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 369..413
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 327..371
id H97426
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 23..259
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..238
id W44834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..120
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 4..54
id R57989
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..154
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 62..91
id R57989
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 112..168
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
TTTGACAGTG CCAMAGCTCG GTACTGGACA CAACGAGGGA CCTGGGTCTA CGATAACGCG      60
CTTTTGCTCC TCCTGAAGTG TCTTTGGTCC AACGTTGTTC CAGASTGTAC C ATG GCT      117
                                     Met Ala

TCC AGT AAC ACT GTG TTG ATG CGG TTG GTA GCC TCC GCA TAT TCT ATT      165
Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile
      -15                      -10                      -5

GCT CAA AAG GCA GGA ATG ATA GTC AGA CGT GTT ATT GCT GAA GGA GAC      213
Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp
      1                      5                      10                      15
```

CTG GGT ATT GTG GAG AAG ACC TGT GCA ACA GAC CTG CAG ACC AAA GCT	261
Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala	
20 25 30	
GAC CGA TTG GCA CAG ATG AGC ATA TGT TCT TCA TTG GCC CGG AAA TTC	309
Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg Lys Phe	
35 40 45	
CCC AAA CTC ACA ATT ATA GGG GAA GAG GAT CTG CCT TCT GAG GAA GTG	357
Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val	
50 55 60	
GAT CAA GAG CTG ATT GAA GAC AGT CAG TGG GAA GAA ATA CTG AAG CAA	405
Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu Lys Gln	
65 70 75	
CCA TGC CCA TCG CAG TAC AGT GCT ATT AAA GAA GAA GAT CTC GTG GTC	453
Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu Val Val	
80 85 90 95	
TGG GTT GAT	462
Trp Val Asp	

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..267
id HSU46357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 291..333
id HSU46357
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 84..128

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 .seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

GCGGGCAGAA AGTTGCCGGA GGTCTCCGGG TGGTATCGCC CTTTCCTCTT TGCCAGCCCG      60
CTGGCGAGCC GAGCCGGGGC AAG ATG AGG TCG TCC TGT GTC CTG CTC ACC GCC      113
      Met Arg Ser Ser Cys Val Leu Leu Thr Ala
      -15                               -10

CTG GTG GCG CTG GCC GCC TAT TAC GTC TAC ATC CCG CTG CCT GGC TCC      161
Leu Val Ala Leu Ala Ala Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser
      -5                               1                               5                               10

GTG TCC GAC CCC TGG AAG CTG ATG CTG CTG GAC GCC ACT TTC CGG GGT      209
Val Ser Asp Pro Trp Lys Leu Met Leu Leu Asp Ala Thr Phe Arg Gly
      15                               20                               25

GCA CAG CAA GTG AGT AAC CTG ATC CAC TAC CTG GGA CTG AGC CAT CAC      257
Ala Gln Gln Val Ser Asn Leu Ile His Tyr Leu Gly Leu Ser His His
      30                               35                               40

CTG CTG GCA CTG AAT TTT ATC ATT GTT TCT TTT GGC AAA AAA AGC GCG      305
Leu Leu Ala Leu Asn Phe Ile Ile Val Ser Phe Gly Lys Lys Ser Ala
      45                               50                               55

TGG TCT TCT GCC CAA GTG AAG GTG ACC GAC ACA GAC TTT GAT GGT GTG      353
Trp Ser Ser Ala Gln Val Lys Val Thr Asp Thr Asp Phe Asp Gly Val
      60                               65                               70                               75

GAA GTC AGA GTG TTT GAA GGC CCT CCG AAG CCC GAA GAG CCA CTG AAA      401
Glu Val Arg Val Phe Glu Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys
      80                               85                               90

CGC AGC GTC GTT TAT ATC CAC GGA RGA GGC TGG      434
Arg Ser Val Val Tyr Ile His Gly Xaa Gly Trp
      95                               100

```

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..266

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..257
 id H10448
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 9..266
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..258
 id HSC18H071
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 21..266
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..246
 id AA127134
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 21..266
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..246
 id HUML13653
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 47..124
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

AGGGATCTGT CGGCTTGTC GGTGGTGGAG GAAAAGGCCG TCCGTC ATG GGG ATC	55
Met Gly Ile	
-25	
CAG ACG AGC CCC GTC CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT	103
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr	
-20 -15 -10	
CTG CTC GGC CTG GCT GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG	151
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg	
-5 1 5	
CCT CAG GTC ACT CTC CTG GAC CCC AAT GAA AAG TAC CTG CTA CGA CTG	199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu	
10 15 20 25	
CTA GAC AAG ACG ACT GTG AGC CAC AAC ACC AAG AGG TTC CGC TTT GCC	247
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala	

CTG CCC ACC GCC CAC CAC ATG
Leu Pro Thr Ala His His Met
45

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 53..91
id N86348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..40
id N86348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 211..241
id N86348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..154
id N88408
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

- (B) LOCATION: 52..258
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: .score 6.3
 seq ILLIVLFLDAVRE/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

AGCGGRSAGC GCAGGGAGCC AGGCGGGCTG CCGGCGGGTG TGAAGAAAAA A ATG ACA      57
                                     Met Thr

CTC CAA TGG GCT GCA GTG GCA ACC TTT CTT TAT GCC GAA ATA GGA CTC      105
Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile Gly Leu
-65                               -60                               -55

ATT TTA ATC TTC TGC CTA CCT TTT ATT CCT CCT CAG AGA TGG CAG AAG      153
Ile Leu Ile Phe Cys Leu Pro Phe Ile Pro Pro Gln Arg Trp Gln Lys
-50                               -45                               -40

ATT TTT TCA TTT AAT GTC TGG GGT AAA ATT GCA ACT TTT TGG AAC AAG      201
Ile Phe Ser Phe Asn Val Trp Gly Lys Ile Ala Thr Phe Trp Asn Lys
-35                               -30                               -25                               -20

GCT TTC CTT ACC ATT ATC ATC CTA TTG ATT GTT CTA TTT CTA GAT GCT      249
Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu Asp Ala
-15                               -10                               -5

GTG AGA GAA GTA AGG AAA TAT TCC TCA GTT CAT ACC ATT GAG AAG AGC      297
Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu Lys Ser
1                               5                               10

TCC ACC AGC AGA CCA AGG                                          315
Ser Thr Ser Arg Pro Arg
15

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 17..138
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..122
 id HSC3DD031
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 137..188
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 120..171
 id HSC3DD031
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 136..188
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 83..135
 id T75196
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 92..139
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 38..85
 id T75196
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 89..343
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq FLDFCVYIPLSWG/FC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

AAGAAGCCTG TGTGGCCTTC CCGGCGGCTG ATTCGAGGGC TTGTTTGGTC AGAAGGGGGG	60
CGTCAGAGAA GCTGCCCCCTT AGCCAACC ATG CCG TCT GAG GGT CGC TGC TGG	112
Met Pro Ser Glu Gly Arg Cys Trp	
-85 -80	
GAG ACC TTG AAG GCC CTA CGC AGT TCC GAC AAA GGT CGC CTT TGC TAC	160
Glu Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr	
-75 -70 -65	
TAC CGC GAC TGG CTG CTG CGG CGC GAG GTG AGC GGT GGC CCC GGA GGA	208
Tyr Arg Asp Trp Leu Leu Arg Arg Glu Val Ser Gly Gly Pro Gly Gly	
-60 -55 -50	
CGT AGG CCT TTC CGG CCC CTC GCG ACC GAA ACC TTC TCC CTA GCC GTT	256
Arg Arg Pro Phe Arg Pro Leu Ala Thr Glu Thr Phe Ser Leu Ala Val	
-45 -40 -35 -30	
GGC ACG TTC TGC TCC CGG GAA CCC GTG CAG TCT AAC AAC CTG CAT TTA	304
Gly Thr Phe Cys Ser Arg Glu Pro Val Gln Ser Asn Asn Leu His Leu	
-25 -20 -15	
TTT CTT GAC TTC TGT GTG TAC ATC CCT CTG TCC TGG GGT TTC TGT CCT	352
Phe Leu Asp Phe Cys Val Tyr Ile Pro Leu Ser Trp Gly Phe Cys Pro	

CTT CAG CCT ATT TTA GCG
Leu Gln Pro Ile Leu Ala

5

370

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 217..302
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 318..391
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 111..182
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..104
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 52..118
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..41

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..30
id N92143
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 119..293
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 91..265
id R97442
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 2..98
id R97442
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 293..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 264..352
id R97442
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(254..378)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..125
id R97398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(146..253)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 125..232
id R97398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(97..147)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 232..282
id R97398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 119..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 90..276
id T80897
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..97
id T80897
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..100
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 119..169
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 93..143
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 246..289
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 219..262
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 203..245
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 175..217
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 142..176
id AA047755
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..116
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq AILGSTWVALTTG/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

AATCCGGGCC GCGCGGGGAA GGGGAGACGT GGGGTAGAGT GACC ATG ACG AAA TTA      56
                                   Met Thr Lys Leu

GCG CAG TGG CTT TGG GGA CTA GCG ATC CTG GGC TCC ACC TGG GTG GCC      104
Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val Ala
-20                               -15                -10                -5

CTG ACC ACG GGA GCC TTG GGC CTG GAG CTG CCC TTG TCC TGC CAG GAA      152
Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln Glu
                               1                   5                   10

GTC CTG TGG CCA CTG CCC GCC TAC TTG CTG GTG TCC GCC GGC TGC TAT      200
Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys Tyr
                               15                   20                   25

GCC CTG GGC ACT GTG GGC TAT CGT GTG GCC ACT TTT CAT GAC TGC GAG      248
Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys Glu
                               30                   35                   40

GAC GCC GCA CGC GAG CTG CAG AGC CAG ATA CAG GAG GCC CGA GCC GAC      296
Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala Asp
                               45                   50                   55                   60

TTA GCC CGC ANG GGC TGC GCT TCT GAC AGC CTA ASC CCA TTC CTG TGC      344
Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa Pro Phe Leu Cys
                               65                   70                   75

GGA CAG CCC TTC CTC CCA TTT CCC ATT AAA GAG CCA GGG      383
Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro Gly
                               80                   85

```

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..205

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 28..189
id AA122029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..44
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..30
id AA122029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..232
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 26..211
id HUML1833
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 113..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..128
id AA158721
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 112..174
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq FLVSNMLLAAYG/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
AAACAAGGGC AGGTCTGACT GCAAGGCTGG GACTGGGAGG CAGAGCCGCC GCCAAGGGGG 60
CCTCGGTAA ACACTGGTCG TTCAATCACC TGCAAGACGA AGGAGGCAAG G ATG CTG 117
                                         Met Leu
                                         -20

TTG GCC TGG GTA CAA GCA TTC CTC GTC AGC AAC ATG CTC CTA GCA GAA 165
Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu Ala Glu
      -15                      -10                      -5

GCC TAT GGA TGT GGA GGC TGT TTC TGG GAC AAC GGC CAC CTG TAC CGG 213
Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu Tyr Arg
      1                      5                      10

GAG GAC CAG ACC TCC CCC GCG CCG GGC CTC CGC TGC CTC AAC TGG CTG 261
Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn Trp Leu
      15                      20                      25
```

GAC GCA CAG AGC GGG
Asp Ala Gln Ser Gly
30

276

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 63..212
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 206..338
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 401..452
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 30..60
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 26..345
id T86800
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 373..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 354..384
id T86800
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 46..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 49..381
id H94753
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..197
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq SVLVLLLLAVLYE/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AGACTCGGAG CGAGGAGACC CGAGCGAGCA GACGCGGCCC TGGCGCCCGC CCTGCGCACT   60
CACC ATG GCG ATG CAT TTC ATC TTC TCA GAT ACA GCG GTG CTT CTG TTT   109
Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe
-40 -35 -30
CAT TTC TGG AGT GTC CAC AGT CCT GCT GGC ATG GCC CTT TCG GTG TTG   157
His Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu
-25 -20 -15
GTG CTC CTG CTT CTG GCT GTA CTG TAT GAA GGC ATC AAG GTT GGC AAA   205
Val Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys
-10 -5 1 5
GCC AAG CTG CTC AAC CAG GTA CTG GTG AAC CTG CCA ACC TCC ATC AGC   253
Ala Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser
10 15 20
CAG CAG ACC ATC GCA GAG ACA GAC GGG GAC TCT GCA GGC TCA GAT TCA   301
Gln Gln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser
25 30 35
TTC CCT GTT GGC AGA ACC CAC CAC AGG TGG TAT TTG TGT CAC TTT GGC   349
Phe Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly
40 45 50
CAG TCT CTA ATC CAT GTC ATC CAG GTG GTC ATC GGC TAC TTC ATC ATG   397
Gln Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met
55 60 65 70

```

CTG GCC GTA ATG TCC TAC AAC ACC TGG ATT TTC CTT GGT GTG GTC
Leu Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val
75 80 85

442

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 183..278
id T97803
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 5..84
id N89398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(300..345)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 273..318
id T97702
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 163..387
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VVXXSVLXTTCXS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGGGGCAGCG CGGGSTCGCC ATGGCTGAGC TGCAGCAGCT CCGGGTGCAG GAGGCGGTGG 60
AGTCCATGGT GAAAGTCTG GAAAGAGAGA ACATCCGGAA GATGCAGGGT CTCATGTTCC 120

```

GGTGCAGCGS CAGCYTGTTK GTVAAAGRMC AGCMAGGCCT CC ATG AAG CAG GTG      174
                               Met Lys Gln Val
                               -75

CAC CAG TGC ATC GAG CGC TGC CAT GTG CCT CTG GCT CAA GCC CAG GCT      222
His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala Gln Ala Gln Ala
-70                               -65                               -60

TTG GTC ACC AGT GAG CTG GAG AAG TTC CAG GAC CGC CTG GCC CGG TGC      270
Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg Leu Ala Arg Cys
-55                               -50                               -45                               -40

ACC ATG CAT TGC AAC GAC AAA GCC AAA GAT TCA ATA GAT GCT GGG WGT      318
Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile Asp Ala Gly Xaa
-35                               -30                               -25

AAG GAG CTT CAG GTG AAG CAG CAG CTG AMA GTT GTG TKR MCA AGT GTG      366
Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val Xaa Xaa Ser Val
-20                               -15                               -10

TTG RTG ACC ACA TGC AMC TCA TCC CAA CTA      396
Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu
-5                               1

```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..179
id AA058587
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..161
id R20025
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 38..125
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 2..89
 id R12128
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 124..193
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 87..156
 id R12128
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 40..193
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 2..155
 id H19999
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 78..193
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..116
 id H83838
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 76..156
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq LLAALMLVAMLQL/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

AAAATCCGGG CTTGCGGCCG CTGGCGTAGT CTGTGGCCGG GTGGTCGTTG CTGCGCGCCC   60
CGAGCCCCGA GAGCC ATG CAG ATG TCC TAC GCC ATC CGG TGC GCC TTC TAC   111
          Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr
          -25                      -20

CAG CTG CTG CTG GCC GCG CTC ATG CTG GTG GCG ATG CTG CAG CTG CTC   159
Gln Leu Leu Leu Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu
-15          -10          -5          1

TAC CTG TCG CTG CTG TCC GGA CTA CAC GGG CCG   192
Tyr Leu Ser Leu Leu Ser Gly Leu His Gly Pro
          5          10

```

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..324
id AA143123
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(192..316)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 312..436
id AA142922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(310..376)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 253..319
id AA142922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(142..191)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 436..485
id AA142922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(130..327)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 7..204
id H54590
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..376

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 10..145
id AA013161
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 241..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 10..145
id AA018245
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..254
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
AAGTAGCAGA GGCAGCTTCT GAGAGCCTGG GCAGGCAGCA GCTGGCTGAC CAAGTCCACT    60
GGAAGAGAAG GCTTGTGCCA GCCGGGAGAA GGAAGCCGGG GACAGGATGR RAGCAACAAC    120
ACCTTTGCAG ACAGTCGACC GGCCCAAGGA CTGGTACAAG ACGATGTTTA AGCAAATTCA    180
CATGGTGCAC AAGCCGG ATG ATG ACA CAG ACA TGT ATA ATA CTC CTT ATA      230
          Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile
          -15                               -10

CAT ACA ATG CAG GTC TGT ACA ACC CAC CCT ACA GTG CTC AGT CAC ACC      278
His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr
          -5                               1                               5

CTG CTG CAA AGA CCC AAR CCT ACA GAC CTC TTT CCA AAA GCC ACT CCG      326
Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
          10                               15                               20

ACA ACA GCC CCA ATG CCT TTA AGG ATG CGT CCT CCC CAG TGC CTC CCC      374
Thr Thr Ala Pro Met Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro
          25                               30                               35                               40

GAG                                                                    377
Glu
```

(2) INFORMATION FOR SEQ ID NO: 179:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 109..425
id AA037143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..110
id AA037143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 443..483
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 423..463
id AA037143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 121..237
id W37233
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..482
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 367..479
id W37233
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 293..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 287..324
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..57
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 15..50
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..128
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 89..122
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 67..96
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 60..89
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 128..424
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 100..396
id N78012
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..128
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 34..101
id N78012
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 417..464
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 390..437
id N78012
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..60
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..32
id N78012
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 107..309
id W52332
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 353..482
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 335..464
id W52332
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..108
id W52332
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 116..305
id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 28..96
id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 95..135
id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 406..441

id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 372..437
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

AGACACTTCC TGGTGGGATC CGAGTGAGGC GACGGGGTAG GGGTTGGCGC TCAGGCGGCG 60
ACCATGGCGT ATCACGGCCT CACTGTGCCT CTCATTGTGA TGAGCGTGT CTGGGGCTTC 120
GTCGGCTTTC TTGGTGCCTT GGTCATCCC TAAGGGTCCT AACCGGGGAG TTATCATTAC 180
CATGTTGGTG ACCTGTTTCT TTTGCTGCTA TCTCTTTTGG CTGATTGCAA TTCTGGCCCA 240
ACTCAACCCT CTCTTTGGAC CGCAATTGAA AAATGAAACC ATCTGGTATC TGAAGTATCA 300
TTGGCCTTGA GGAAGAAGAC ATGCTCTACA GTGCTCAGTC TTTGAGGTCA CGAGAAGAGA 360
ATGCCTTCTA G ATG CRN DAT CAC CTC CAA ACC AGA CCA CTT TTC TTG ACT 410
          Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr
          -20                      -15                      -10

TGC CTG TTT TGG CCA TTA GCT GCC TTA AAC GTT AAC AGC ACA TTT GAA 458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
          -5                      1                      5

TGC CTT ATT CTA CAA TGC AGC GTG GGG ATC 488
Cys Leu Ile Leu Gln Cys Ser Val Gly Ile
          10                      15

```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 139..237
id T53688
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..175
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 74..146
id T53688
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 179..334
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LMAFLLSFYLIPT/NE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

AATGCGCAGA AACACTGGGC ACAGGGGGAG GTAAC TGCAG TAAGTCCCGC TTGGCCCTGG      60
AGTCCACGCG GATTTTCGAA GCTGGGGCTG GCAAGAGGCC GCTGGACACC ACGCTCCACT      120
CGTCAGCCCA CTTCTAGCT GAACAGCGCG AGGCGGCGGC AGCGAGCCGG GTCCCACC      178
ATG GCC GCG AAT TAT TCC AGT ACC ART ACC CGG AGA GAA CAT GTC AAA      226
Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys
      -50                      -45                      -40

GTT AAA ACC AGC TCC CAG CCA GGC TTC CTG GAA CGG CTG AGC GAG ACC      274
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
      -35                      -30                      -25

TCG GGT GGG ATG TTT GTG GGG CTC ATG GCC TTC CTG CTC TCC TTC TAC      322
Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
      -20                      -15                      -10                      -5

CTA ATT TTC ACC AAT GAG GGC CGC GCA TTG AAG ACG GCA ACC TCA TTG      370
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
              1                      5                      10

GCT GAG GGG CTC TCG CTT GTN GTG TCT CCC GAC AGC ATC CAC AGT GTG      418
Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
              15                      20                      25

GCT CCG GAG AAT GAA GGA ANG CTG GTG CAC ATC ATT      454
Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile
              30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..215
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 227..309
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(60..284)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 216..440
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(287..329)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 172..214
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..139
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 183..248
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 84..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..131
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 247..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 165..247
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 253..315
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq LEMLTAFASHIRA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```
AACGAGTTCT TCCGGGGCGG AGGTCACCAT GGCAGCTGCC TTGGCTCGGC TTGGTCTGCG 60
GCCTGTCAAA CAGGTTCTGG TTCAATTCTG TCCCTTCGAG AAAAACGTGG AATCGACGAG 120
GACCTTCCTG CAGACGGTGA GCAGTGAGAA GGTCCGCTCC ACTAATCTCA ACTGCTCAGT 180
GATTGCGGAC GTGAGGCATG ACGGCTCCGA GCCCTGCGTG GACGTGCTGT TCGGAACGGG 240
CATCGCCTGA TT ATG CGC GGC GCT CAT CTC ACC GCT CTG GAA ATG CTC ACC 291
      Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr
      -20              -15              -10

GCC TTC GCC TCC CAC ATC CGG GCC AGG GAC GCA TCG GGG 330
Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ser Gly
      -5              1              5
```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 228..367

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 143..282
id AA143123
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 89..206
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..118
id AA143123
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(228..360)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..139
id H54590
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(166..206)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 164..204
id H54590
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(201..349)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 312..460
id AA142922
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..367
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 10..103
id AA013161
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..367
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 10..103
id AA018245
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 216..287
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```
AAGTGTATCT GGGCAGCCCC TTCCGGCAAA ACGCAGCAGT AGCAGAGGCA GCTTCTGAGA    60
GCCTGGGCAG GCAGCAGCTG GCTGACCAAG TCCACTGGAA GAGAAGGCTT GTGCCAGCCG   120
GGAGAAGGAA GCCGGGGACA GGATGAAAGC AACAAACACCT TTGCAGACAG TCGACCGGCC   180
CAAGGACTGG TACAAGACGA TGTTAAGCAA TTCAC ATG GTG CAC AAG CCG ATG       233
                                   Met Val His Lys Pro Met
                                   -20

ATG ACA CAG ACA TGT ATA ATA CTC CTT ATA CAT ACA ATG CAG GTC TGT     281
Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val Cys
-15                               -10                               -5

ACA ACC CAC CCT ACA GTG CTC AGT CAC ACC CTG CTG CAA AGA CCC AAA     329
Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro Lys
      1                5                10

CCT ACA GAC CTC TTT CCA AAA GCC ACT CCG ACA ACA                     365
Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr
  15                20                25
```

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 85..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 85..197
id N43024
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..85
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92

region 17..84
id N43024
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 97..189
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 80..172
id T62095
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..96
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 35..80
id T62095
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..35
id T62095
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 26..172
id W42796
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 114..211
id AA030227
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 51..148
id AA118270
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..177

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq IGLMFLMLGALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```
GTGTGCTGGC CGCCGTAGCG CGTCTTGGGT CTCCCGGCTG CCGCTGCTGC CGCCGCCGCC      60
TCGGGTCGTG GAGCCAGGAG CGACGTCACC GCC ATG GCA GGC ATC AAA GCT TTG      114
                               Met Ala Gly Ile Lys Ala Leu
                               -25

ATT AGT TTG TCC TTT GGA GGA GCA ATC GGA CTG ATG TTT TTG ATG CTT      162
Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe Leu Met Leu
-20                               -15                               -10

GGA TGT GCC CTT CCA ATA TAC AAC AAA TAC TGG CCT ACG      201
Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Thr
-5                               1                               5
```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..268
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 119..252
id W20516
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..92
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 12..79
id W20516
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 352..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 343..382

id W20516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 401..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 393..425
id W20516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..122
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 79..108
id W20516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 203..471
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 420..688
id HSZ78368
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..106
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 46..124
id HSZ78368
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..204
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 151..220
id HSZ78368
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..303
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 132..300
id R82255
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..106
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 24..105
id R82255
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..31
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 2..31
id R82255
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 205..471
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..321
id H99530
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 203..358
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 391..546
id AA209097
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 208..270
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

AAGAGGGGAA CAAGATGGCG GCGCCGAAGG GGAGCCTCTG GGTGAGGACC CAACTGGGGC   60
TCCCGCCGCT GCTGCTGCTG ACCATGGCCT TGGCCGAGG TTCGGGGACC GCTTCGGGCTG  120
AAGCATTGGA CTCGGKCYTG GGKKRATACG GCGTCTTGCC ACCGGGCCTG TCAGTTGACC   180
TACCCCTTGC ACACCTACCC TAAGCTT ATG TCC CTG ATG CCA AAA ATG CAC CTA   234
                               Met Ser Leu Met Pro Lys Met His Leu
                               -20                               -15

CTC TTT CCT CTA ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC   282
Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp
                               -10                               -5                               1

TCC GCA CAG AGC TTC ATA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC   330
Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala
                               5                               10                               15                               20

GAT GAC GGR AAA ATA GTT ATA TTC CAG TCT AAG CCA GAA ATC CAG TAC   378

```

```

Asp Asp Gly Lys Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr
      25                      30                      35
GCA CCA CAT TTG GAG CAG GAG CCT ACA AAT TTG AGA GAA TCA TCT CTA      426
Ala Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu
      40                      45                      50
AGC AAA ATG TCC TAT CTG CAA ATG AGA AAT TCA CAA GCG CAC AGG      471
Ser Lys Met Ser Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg
      55                      60                      65

```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 123..407
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 69..119
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 38..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq SNILLASVGSVLG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

ATTTCCTGGG CCAAGTTGGG ACCCGGACGG CCTCACC ATG ATG AAA CGG GCA GCT      55
                               Met Met Lys Arg Ala Ala
                               -85
GCT GCT GCA GTG GGA GGA GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG      103
Ala Ala Ala Val Gly Gly Ala Leu Ala Val Gly Ala Val Pro Val Val

```

-80	-75	-70	
CTC AGT GCC ATG GGC TTC ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA			151
Leu Ser Ala Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile			
-65	-60	-55	-50
GCA GCC AAG ATG ATG TCC GCA GCA GCC ATT GCC AAC GGG GGT GGT GTT			199
Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val			
-45	-40	-35	
TCT GCG GGG AGC CTG GTG GCT ACT CTG CAG TCC GTG GGG GCA GCT GGA			247
Ser Ala Gly Ser Leu Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly			
-30	-25	-20	
CTC TCC ACA TCA TCC AAC ATC CTC CTG GCC TCT GTT GGG TCA GTG TTG			295
Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu			
-15	-10	-5	
GGG GCC TGC TTG GGG AAT TCA CCT TCH KCT TCT CTC CCA GCT GAA CCC			343
Gly Ala Cys Leu Gly Asn Ser Pro Ser Xaa Ser Leu Pro Ala Glu Pro			
1	5	10	15
GAB GKN DAA GAA GAT GAG GCA AGA GAA AAT GTA CCG CCG			382
Xaa Xaa Xaa Glu Asp Glu Ala Arg Glu Asn Val Pro Pro			
20	25		

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 102..301
id H10706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 6..101
id H10706
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 74..273
id AA043571
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 42..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..73
id AA043571
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 99..298
id W63643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 18..98
id W63643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 38..237
id AA081648
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..265
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 89..236
id HUMHBC2885
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..87
id HUMHBC2885
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 220..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq VTIILLSCXFWA/VK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
AAAGTAGGGC TGGCGTASGG CCGCCATGTT GCAGCAGGAT AGTAATGATG AACTGAAGA   60
TGTTTCACTG TTTGATGCGG AAGAGGAGAC GACTAATAGA CCAAGRWAAG CCRAVDRRTC  120
AGRCGTCCAG TAGCRTCGTT TTTCCACTTA TTCTTTCGAG TCAGTGCAAT SATCGTCTAT  180
CTTCTCTGTG AGTTGSTCAG CAGCAGCTTT ATTACCTGT ATG GTG ACA ATT ATC      234
                                   Met Val Thr Ile Ile
                                   -10

TTG TTG TTG TCG TGT GRC TTT TGG GCA GTG AAG AAT GTC ACA KGT AGA      282
Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys Asn Val Thr Xaa Arg
                                   -5              1              5

SKA ATG GTT GGC CTA CGT TGG TGG AAT CAC ATT                          315
Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile
                                   10              15
```

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 123..447
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 69..119
id W52706

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 14..274
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

AGACGGCCTC ACC ATG AWR AAA CGG GCA GCT GCT GCT GCA GTG GGA GGA      49
      Met Xaa Lys Arg Ala Ala Ala Ala Val Gly Gly
      -85                                -80

GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC ATG GGC TTC      97
Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe
-75                                -70                                -65                                -60

ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC AAG ATG ATG TCC      145
Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser
      -55                                -50                                -45

GCA GCA GCC ATT GCC AAC GGG GGT GGT GTT TCT GCG GGG AGC CTG GTG      193
Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val
      -40                                -35                                -30

GCT ACT CTG CAG TCC GTG GGG GCA GCT GGA CTC TCC ACA TCA TCC AAC      241
Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn
      -25                                -20                                -15

ATC CTC CTG GCC TCT GTT GGG TCA GTG TCG GGG GCC TGC TTG GGG AAT      289
Ile Leu Leu Ala Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn
      -10                                -5                                1                                5

TCA CCT TCT TCT TCT CTC CCA GCT GAA CCC GAG GCT AAA GAA GAT GAG      337
Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu
      10                                15                                20

GCA AGA GAA AAT GTA CCC CAA GGT GAA CCT CCA AAA CCC CCA CTC AAG      385
Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys
      25                                30                                35

TCA GAG AAA CAT GAG CGG      403
Ser Glu Lys His Glu Arg
      40

```

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 86..352
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq DLSLLSLPPGTS⁺P/VG

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 188:

AGGCGGCATT	TCCGGCCGGC	GCCAGGGTGG	AGAGTTGTGC	GCCGGTCCCT	GGGCCTGAGC		60
TCCGGCTCCG	GCTGGGGCGC	CTGCG	ATG TCT CAA GAT	GGC GGA STG GGC	GAA	112	
			Met Ser Gln Asp	Gly Gly Xaa Gly	Glu		
				-85			
TTA AAG CAC ATG GTG ATG AGT TTC CGG GTG TCT GAG CTC CAG GTG CTT						160	
Leu Lys His Met Val Met Ser Phe Arg Val Ser Glu Leu Gln Val Leu							
-80			-75		-70	-65	
CTT GGC TTN SCT GGC CGG AAC AAG AGT GGA CGG AAG CAC GAG CTC CTG						208	
Leu Gly Xaa Xaa Gly Arg Asn Lys Ser Gly Arg Lys His Glu Leu Leu							
			-60		-55	-50	
GCC AAG GCT CTG CAC CTC CTG AAG TCC AGC TGT GCC CCT AGT GTC CAG						256	
Ala Lys Ala Leu His Leu Leu Lys Ser Ser Cys Ala Pro Ser Val Gln							
			-45		-40	-35	
ATG AAG ATC AAA GAG CTT TAC CGA CGA CGC TTT CCC CGG AAG ACC CTG						304	
Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu							
			-30		-25	-20	
GGG CCC TCT GAT CTC TCC CTT CTC TCT TTG CCC CCT GGC ACC TCT CCT						352	
Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro							
			-15		-10	-5	
STA GGC TCC CCT GGT CCT CTA GCT CCC ATT CCC CCA ACG STG TTG GCK						400	
Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Xaa Leu Ala							
1			5		10	15	

STG GCA MCC TGC TGG GCC CCA AGC GTG AGG TGG ACA TGC
Xaa Ala Xaa Cys Trp Ala Pro Ser Val Arg Trp Thr Cys
20 25.

439

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 127..268
id W31492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..101
id W31492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 331..376
id W31492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..151
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..134
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 237..297
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 293..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 187..237
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 234..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 119..228
id H52756
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 20..126
id H52756
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..405
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 228..291
id H52756
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..118
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 234..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 111..220
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..385

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 220..263
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..119
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 288..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 167..222
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 222..265
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 268..339
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LLLPRVLLTMASG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
AAATCACGTG GCTGCCACCC AGGTAAGAAG AGGCCGCTCT TCCTGGGGTT GTTCTCCGT 60
GTGACGTGTG GCCTTTGAGA TCAACTCTCC TGTACCAGCG TAGGCCGCAT GAGTGGGGG 120
CGGGCTCCCG CGGTCCTGCT CGGCGGAGTG GTGAGTGACC GGCCCCGCCC CGCCCCTTCC 180
GGTCCTCGAA GCCTCGACCG CTACCCGCAC CCTAAATCCC AGAGGTTGGC CCCCTGAGGT 240
GCCTCTCTGC TCCTGTCTTT TGTTTGG ATG CCG GMG CTG CTG CCT GTG GCC TCM 294
Met Pro Xaa Leu Leu Pro Val Ala Ser
-20

CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC 342
Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
-15 -10 -5 1

CTC CGA CYC AGC VCT CGM CGG CCT CGG ATT CCG GMT CTG GCT ACG TTC 390
Leu Arg Xaa Ser Xaa Arg Arg Pro Arg Ile Pro Xaa Leu Ala Thr Phe
```

CGG GMT CGG TCT CTG
Arg Xaa Arg Ser Leu
20

405

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 54..373
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..73
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 4..251
id HSC3GD011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 270..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 29..166
id HSC01E081
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 243..274
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: . identity 96
 region 1..32
 id HSC01E081
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 337..407
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..71
 id T05865
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 42..146
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq IFSFLDIIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

GTGTGACTTC GGGCTGTGGG CTCGCTCGCG GCTCTTCGGC C ATG GTT TTC TCA AAC	56
Met Val Phe Ser Asn	
-35	
AAT GAT GAA GGC CTT ATT AAC AAA AAG TTA CCC AAA GAA CTT CTG TTA	104
Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu Leu Leu Leu	
-30 -25 -20 -15	
AGA ATA TTT TCC TTC TTG GAT ATA GTA ACT TTG TGC CGA TGT GCA CAG	152
Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg Cys Ala Gln	
-10 -5 1	
ATT TYM AAG GCT TGG AAC ATC TTA GCC CTG GAT GGA AGC AAC TGG CAA	200
Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser Asn Trp Gln	
5 10 15	
AGA ATA GAT CTT TTT AAC TTT CAA ACA GAT GTA GAG GGT CGA GTG GTG	248
Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val Glu Gly Arg Val Val	
20 25 30	
GAA AAT ATC TCG AAG CGA TGC GGT GGA TTC CTG AGG AAG CTC AGC TTG	296
Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu Arg Lys Leu Ser Leu	
35 40 45 50	
CGA GGC TGC ATT GGT GTT GGG GRT TCC TCC TTG RAG ACC TTT GCA CAG	344
Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu Xaa Thr Phe Ala Gln	
55 60 65	
AAC TGC CGA AAC ATT GAA CAT TTG AAC CTC AAT GGA TGC ACA AAA ATC	392
Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys Thr Lys Ile	
70 75 80	
ACT GRC AGC ACG TGT	407
Thr Xaa Ser Thr Cys	
85	

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..202
id HSC3GD011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 54..175
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..73
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 67..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
AAGGACAACG GCGCTCGCMR GCGCCGTGTG ACTTCGGGCT GTGGGCTCGC TCGCGGCTCT   60
TCGGCC ATG GTT TTC TCA AAC AAT GAT GAA GGC CTT ATT AAC AAA AAG   108
Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys
-35          -30          -25
TTA CCC AAA GAA CTT CTG TTA AGA ATA TTT TCC TTC TTG GAT ATA GTA   156
```

Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
-20 -15 -10

ACT TTG TGC CGA TGT GCA CAG ATT TCC AAG GCT TGG AAC ATC TTA GCC 204
Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
-5 1 5 10

CTG GAT GGA AGC AAC TGG CAG GGG 228
Leu Asp Gly Ser Asn Trp Gln Gly
15

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 36..323
id W44483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 305..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 317..410
id W44483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 398..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 411..460
id W44483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(181..321)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 233..373
id AA035386

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(323..447)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 108..232
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(109..184)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 371..446
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(10..64)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 494..548
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(77..112)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 444..479
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..420
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 12..417
id H69070
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 416..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 414..444
id H69070
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..257
id AA057029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..447
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 292..434
id AA057029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..447
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 167..434
id W32750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..185
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..171
id W32750
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 18..353
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq SSCILPWLSKTNS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

AAGAAGGCTG GGCAGCC ATG GCG TCC TAT TTC GAT GAA CAC GAC TGC GAG	50
Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu	
-110 -105	
CCG TCG GAC CCT GAG CAG GAG ACG CGA ACC AAC ATG CTG CTG GAG CTC	98
Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu	
-100 -95 -90	
GCA AGG TCA CTT TTC AAT AGG ATG GAC TTT GAA GAC TTG GGG TTG GTA	146
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val	
-85 -80 -75 -70	
GTA GAT TGG GAC CAC CAC CTG CCT CCA CCA GCT GCC AAG ACT GTG GTT	194
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val	
-65 -60 -55	
GAG AAC CTC CCC AGG ACA GTC ATC AGA GGC TCT CAG GCT GAG CTC AAG	242
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys	
-50 -45 -40	

TGC CCC GTG TGT CTT TTG GAA TTT GAG GAG GAG GAG ACT GCC ATT GAG	290
Cys Pro Val Cys Leu Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu	
-35 -30 -25	
ATG CCT TGC CAT CAC CTT TTC CAT TCC AGC TGC ATT CTG CCC TGG CTA	338
Met Pro Cys His His Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu	
-20 -15 -10	
AGC AAG ACA AAT TCC TGT CCC TTG TGC CGC TAT GAG CTG CCC ACT GAT	386
Ser Lys Thr Asn Ser Cys Pro Leu Cys Arg Tyr Glu Leu Pro Thr Asp	
-5 1 5 10	
GAC GAC ACT TAT GAG GAG CAC AGA CGA GAT AAG GCT CGA AAA CAG CAG	434
Asp Asp Thr Tyr Glu Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln	
15 20 25	
CAG CAA CAC CGA CCA NGG	452
Gln Gln His Arg Pro Xaa	
30	

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 12..404
id W22200
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..332
id R87595
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 96..309
id AA031849

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..123
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 110..286
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..123
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..112
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 49..303
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 74..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..53
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 253..297
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

AAAAAGGGG AGGAAATTGA AACTGAGTGG CCCACGATGG GAAGAGGGGA AAGCCCAGGG 60

GTACAGGAGG CCTCTGGGTG AAGGCAGAGG CTAACATGGG GTTCGGAGCG ACCTTGCCG 120

```

TTGGCCTGAC CATCTTTGTG CTGTCTGTCG TCACTATCAT CATCTGCTTC ACCTGCTCCT 180
GCTGCTGCCT TTACAAGACG TGCCGCCGAC CACGTCCGGT TGTCACCACC ACCACATCCA 240
CCACTGTGGT GC ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT 291
      Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala
      -15                -10                -5

ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG 339
Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln
      1                5                10

GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT ACC CAC CAC CTT ACC CAG 387
Gly Cys Gln Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln
      15                20                25                30

CCC AGC CCA TGG GCC CAC CGG SCT ACC ACG AGA CCC TGG CTG GAG GAG 435
Pro Ser Pro Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu
      35                40                45

CAG CCG CGC CCC GGG 450
Gln Pro Arg Pro Gly
      50

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 85..139
id AA157672
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 86..140
id AA157671
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..94

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 10..47
id HUML116
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..263
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LRRLGCLTLTSL/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATTGCGTAG TTCCGAATAC CCTCGGCCAC ACCTGGCCTT CTCC ATG CTC GGA ATA 56
Met Leu Gly Ile
-70

ACT TCC TGC AGC GAC CAA CAG GCT AAA GAG GGG GAA GGT CTG GAG GGA 104
Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu Gly Leu Glu Gly
-65 -60 -55

TCC AGC ACC GGC TCC TCC TCC GGC AAC CAC GGT GGG AGC GGC GGA GGA 152
Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly
-50 -45 -40

AAT GGA CAT AAA CCC GGG TGT GAA AAG CCA GGG AAT GAA GCC CGC GGG 200
Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly
-35 -30 -25

AGC GGG AAT CTG GGA TTC AGA ACT CTG AGA CGT CTC CTG GGA TGT TTA 248
Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu Leu Gly Cys Leu
-20 -15 -10

ACT TTG ACA CTT TCT GGA AGA ATT 272
Thr Leu Thr Leu Ser Gly Arg Ile
-5 1

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91

region 190..271
id AA103102
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..108
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 143..191
id AA103102
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 72..122
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq ALKLASWTSMALA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

AAATTCCCCG CTACCGGGTT GCGGCCGGAA GCCGGGCGCC GCGGCTCTGC TTCCTCGGG      60
GATCTGGCGA C ATG GCC AGA AAG GCT CTC AAG CTT GCT TCG TGG ACC AGC      110
      Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser
                -15                -10                -5
ATG GCT CTT GCT GCC TCT GGC ATC TAC TTC TAC AGT AAC AAG TAC TTG      158
Met Ala Leu Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu
                1                5                10
GAC CCT AAT GAC TTT GGC GCT GTC AGG GTG GGC AGA GCA GTT GCT ACG      206
Asp Pro Asn Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr
                15                20                25
ACG GCT GTC ATC AGT KAC GAC TAC CTC ACT TCC CTG AAG AGT GTC CCT      254
Thr Ala Val Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro
                30                35                40
TAT GGC TCA GAG GAG TAC TTG CAG CTG AGA TCT AAG GTG CAC CTT CGC      302
Tyr Gly Ser Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg
                45                50                55                60
TCT GCC AGG CGT CTC TGT NAR STC TGC TGT GCC AAC CGG GGC      344
Ser Ala Arg Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
                65                70

```

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..394
id AA284513
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..332
id H99096
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 355..395
id H99096
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..359
id AA020823
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 17..396
id N21197
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 11..277
id AA083141
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..57

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 .seq AALPAWLSLQSR/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

CTCGCAGCC ATG GCG GCC GCC GCG CTC CCA GCA TGG CTG TCT CTG CAG TCG	51
Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser	
-15 -10 -5	
AGG GCA AGG TCT CTG CGT GCA TTC TCC ACT GCC GTC TAC TCG GCC ACT	99
Arg Ala Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr	
1 5 10	
CCG GTC CCG ACA CCT AGC CTG CCG GAA AGA ACA CCC GGA AAT GAA AGG	147
Pro Val Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg	
15 20 25 30	
CCA CCA AGN AGA AAG GCA CTA CCT CCT AGG ACA GAG AAA ATG GCT GTT	195
Pro Pro Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val	
35 40 45	
GAC CAG GAC TGG CCT AGT GTT TAC CCA GTT GCA GCA CCA TTB AAA CCC	243
Asp Gln Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro	
50 55 60	
TCT GCA GTA CCT CTT CCT GTT CGA ATG GGT TAT CCA GTA AAA AAG GGC	291
Ser Ala Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly	
65 70 75	
GTG CCC ATG GCA AAG GAG GGA AAT CTA GAA CTT TTA AAG ATT CCC AAT	339
Val Pro Met Ala Lys Glu Gly Asn Leu Glu Leu Lys Ile Pro Asn	
80 85 90	
TTT CTG CAT TTG ACT CCT GTA GCA ATT AAA AAG CAC TGT GNR GCC CTT	387
Phe Leu His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu	
95 100 105 110	
AAA GAT TTT TGC ACT GAG	405
Lys Asp Phe Cys Thr Glu	
115	

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 92..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: . identity 97
region 83..446
id W37917
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 5..85
id W37917
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..446
id AA010474
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..84
id AA010474
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 79..289
id W77834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 368..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 345..432
id W77834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..106
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 6..80
id W77834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 288..349
id W77834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 85..374
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 3..74
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 389..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 370..436
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 183..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 158..430
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..66
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 114..164
id AA169869

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 104..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 77..117
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..312
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CMLTLXXLSFILA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

GTAGTGTTAG ACTGAAGATA AAGTAAGTGC TGTTTGGGCT AACAGGATCT CCTCTTGCAG      60
TCTGCAGCCC AGGACGCTGA TTCCAGCAGC GCCTTACCGC GCASCCGAAG ATTCACT      117
ATG GTG AAA ATC GCC TTC AAT ACC CCT ACC GCC GTG CAA AAG GAG GAG      165
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65                -60                -55                -50
GCG CGG CAA GAC GTG GAG GCC CTC CTG AGC CGC ACG GTC AGA ACT CAG      213
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
-45                -40                -35
ATA CTG ACC GGC AAG GAG CTC CGA GTT GCC ACC CAG GAA AAA GAG GGC      261
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
-30                -25                -20
TCC TCT GGG AGA TGT ATG CTT ACT CTC TTN NVC CTT TCA TTC ATC TTG      309
Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
-15                -10                -5
GCA GGA CTT ATT GTT GGT GGA GCC TGC ATT TAC AAG TAC TTC ATG CCC      357
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
1                5                10                15
AAG AGC ACC ATT TAC CGT GGA NAG ATG TGC TTT TTT GAT TCT GAG GAT      405
Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
20                25                30
CCT GCA AAT TCC CTT CGT GGA GGA GAG CCT AAC TTC CTG CCT GTG ACT      453
Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
35                40                45

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Thyroid

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 11..171

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 1..161
id HUM085F04B
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 9..109

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..101
id AA143653
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(62..155)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 24..117
id H17554
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 103..185

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 139..221
id H18908
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 109..185

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 133..209
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 11..154

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq LLLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

AAACCGCGGCC ATG ATA GGG TCG GGA TTG.GCT GGC TCT GGA GGC GCA GGT      49
      Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly
                -45                                -40

GGT CCT TCT TCT ACT GTC ACA TGG TGC GCG CTG WTT TCT AAT CAC GTG      97
Gly Pro Ser Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val
-35                -30                                -25                                -20

GCT GCC ACC CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG      145
Ala Ala Thr Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
                -15                                -10                                -5

CTG CTG CCT GAT GGC CTC CCG CCW TTT GTT GCT ACC CCG ATG      187
Leu Leu Pro Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
      1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 202..319
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 316..406
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 167..284
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 281..364
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..137
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..296
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 213..292
id W25483

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..132
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 307..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 177..294
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 329..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 288..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 313..366
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LXGFLFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```
AATAACTGAA AGTAGCTAAG GCACCCAGC CGGAGGAAGT GAGCTCTCCT GGGGCGTGGT   60
TGTTCTGTGAT CCTTGCATCT GTTACTTAGG GTCAAGGCTT GGGTCTTGCC CCGCAGACCC  120
TTGGGACGAC CCGGCCCCAG CGCASTATGA ACCTGGAGCG AGTGTCCAAT GAGGAGAAAT  180
TGAACCTGTG CCGGAAGTAC TACCTGGGGG GGTITGCTTT CCTGCCTTTT CTCTGGTITG  240
TCAACATCTT CTGTTCTTTC CGAGAGGCCT TCCTTGTCCT AGCCTACACA GAACAGAGCC  300
AAATCAAAGG CT ATG TCT GGC GCT CAG CTK HTG GGC TTC CTC TTC TGS GTG  351
      Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val
      -15                               -10

ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC CGC   399
Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg
-5          1          5          10

TGG GGG TGC CCT TGG GGA CTA CCT CTC CTT CAC ATA CCC CTG GGC ACC   447
Trp Gly Cys Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr
      15          20          25

CCT GAC AAC TTC TGC ACA TAC   468
Pro Asp Asn Phe Cys Thr Tyr
      30
```

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Placenta

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 328..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 15..119
id HUMGS01778
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(256..309)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 175..228
id HSAAAAJHX
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 188..274
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq VVFMTVARSGASS/FA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

ACGGTTCCGG GCGTTACCAT CGTCCGTGCG CACCGCCCGG CGTCCAGGTG AGTCTCCCAT   60
CTGCAGAGAC GCGGACGCGC CGGCCCGCAG TTGGCCTGCG GACGCGGTGG ACGGTTTGGC   120
GCCCACCAGG CGATCAATAC TTTGGATTTT TAATTTCTAG ATTTGGCAAT TCTTCGCTGA   180
AGTCATC ATG AGC TTT TTC CAA CTC CTG ATG AAA AGG AAG GAA CTC ATT   229
  Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile
                    -25                      -20

CCC TTG GTG GTG TTC ATG ACT GTG GCG GCG AGT GGA GCC TCA TCT TTC   277
Pro Leu Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe
-15                      -10                      -5                      1

GCT GTG TAT TCT CTT TGG AAA ACC GAT GTG ATC CTT GAT CGA AAA AAA   325
Ala Val Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys
                    5                      10                      15

AAT CCA GAA CCT TGG GAA ACT GTG GAC CCT ACT GTA CCT CAA AAG CTT   373
Asn Pro Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu
                20                      25                      30

ATA ACA ATC AAC CAA CAA TGG AAA CCC ATT GAA GAG TTG CAA AAT GTC   421
Ile Thr Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val
                35                      40                      45

CAA AGG GTA ACG   433
Gln Arg Val Thr
50

```

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..242)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..215
id N91097
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 103..147
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

GCGGGAGGTG GGGCATCCGG GTCTCTTGGT GGCTGCTTCT ACCCCCGGAG CTCAGCTGAT   60
CTTCCCTTCC AGACTACGAG GTGTGAATTT CAAACTTCCG TA ATG GAG TTA GCC   114
                               Met Glu Leu Ala
                               -15
CAC AGT TTA TTG CTA AAT GAA GAA GCT TTG GCT CAA ATC ACC GAA GCA   162
His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln Ile Thr Glu Ala
-10                               -5                               1                               5
AAA AGA CCA GTT TTC ATC TTT GAA TGG TTG CGA TTT CTT GAT AAA GTC   210
Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe Leu Asp Lys Val
                               10                               15                               20
TTG GTT GCT GCC AAC AAG ACC GAT GTA AAG GAA AAA CAG AAA AAA CTT   258
Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys Gln Lys Lys Leu
                               25                               30                               35
GTT GAA CAA TTA ACT GGA TTA ATA AGT AGT TCA CCT GGA CCC ACC GGG   306
Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro Gly Pro Thr Gly
                               40                               45                               50

```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..331
id H23844
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 21..332
id H22656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 8..306
id AA036876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..183
id W05714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 183..293
id W05714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..322

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
 region 1..283
 id R69117
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..139
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
 seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```
CTGAAGCCGG AAGCTACCTA TCTGGTAGGG AGCTCCCCCA GCACCGAAGA CTGCG ATG      58
                                         Met

ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC CAG CTC GGC      106
Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu Gly
   -25                      -20                      -15

TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT GGG GAC CTG      154
Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp Leu
   -10                      -5                      1                      5

GAG AAT GAT GAG CAG GCA GCC AGT GCC ATC TCT GAG CTG GTC AGC ACA      202
Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser Thr
           10                      15                      20

GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC TTC AAG CGC      250
Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys Arg
           25                      30                      35

CTG TCT GTG GTC TTT GGA GAA CAC ACA CTG CTG GTG ACG GTG TCA GGA      298
Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser Gly
           40                      45                      50

CAG AGG GTG TTT GTG GTG AAG AGG GGG      325
Gln Arg Val Phe Val Val Lys Arg Gly
           55                      60
```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..374
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 125..358
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..119
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 388..452
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 374..438
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 131..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 113..315
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..137
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 43..120
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 323..374
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 304..355
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 388..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 371..416
id AA143062
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..317
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 388..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 370..416
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 8..46
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..359
id HUM159G08B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..47
id HUM159G08B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..316
id N34957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 30..97
id N34957

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 12..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LVGVLFVSVTTG/PW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

AGGTCTCCAA G ATG GCG GCC GCC TGG CCG TCT GGT CCG KCT GCT CCG GAG      50
      Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
            -30                -25                -20

GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC TCA GTC ACT      98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
            -15                -10                -5

ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC GAG GAG TCG      146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
            1                5                10

CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT AAA GAT CCA      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
            15                20                25                30

AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA AAC TAC ACA      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
            35                40                45

GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT AAG GAT NCC      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa
            50                55                60

AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT TTT TTC AAG      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
            65                70                75

CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC NNT KAG CAG TNN      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa
            80                85                90

NWT GTC TCT TTT TCT TGG ATG GTT GGG AGC AGA TCG ATT TTA CCT TGG      434
Xaa Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
            95                100                105                110

ATA CCC TGC TTT GGG TTT GTT      455
Ile Pro Cys Phe Gly Phe Val
            115

```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 157..188
id AA102919
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 117..155
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```
AAGCAGCTGG ATCTCCGGTA ACTGAGACAT AGGGTATAAC TGTGTGTCGG GCGGAGGAAG      60
TGAGGACGGC GCCAAGGGCC TTCCGGGCCA GTGTTGGATC CCTGTAGTTT GTGAAG ATG      119
                                         Met
GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG GAC GGG CTC CCG CTG GCC      167
Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu Ala
   -10                -5                1
GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC CGG                        200
Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
   5                10                15
```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 57..372

id AA023107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 194..436
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 157..399
id AA102919
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 141..179
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

AACCTCAGCG GGAAGCGGAG ACGCAAGCAG CTKGATCTCC GGTAAGTGA ACATAGGGTA    60
TAACTGTTGT CGCGGCGGAG GAAGTGAGGA CGGCGCCAAG GGCCTTCCGG GCCASTGTTG   120
GATCCCTGTA GTTTGTGAAG ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG   173
          Met Val Leu Leu Thr Met Ile Ala Arg Val Ala
                      -10                      -5

GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC   221
Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly
          1                      5                      10

CGG GAC CTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA AAG   269
Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys
          15                      20                      25                      30

TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC ATG   317
Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met
          35                      40                      45

ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA TGT   365
Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys
          50                      55                      60

GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT TTG   413
Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu
          65                      70                      75

CAC TCA GAA TTT GAT GAA CAG   434
His Ser Glu Phe Asp Glu Gln
          80                      85

```

(2) INFORMATION FOR SEQ ID NO: 206:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 base pairs
(B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 86..333
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 7..81
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 349..378
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..288
id R97144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..94
id R97144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 63..353
id H64963

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 38..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..58
id H64963
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..392
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 32..322
id W03796
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 86..340
id N73170
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 3..81
id N73170
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 117..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq MMVLSLGIXLASA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
AAGAAGATGA AGGTAAGTAG AAACCGTTGA TGGGACTGAG AAACCAGAGT TAAAACCTCT    60
TTGGAGCTTC TGAGGACTCA GCTGGAACCA AMCGGGCACA GGTGGCAAC ACCATC ATG    119
                                         Met
ACA TCA CAA CCT GTT CCC AAT GAG ACC ATC ATA GTG CTC CCA TCA AAT    167
Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser Asn
      -65                      -60                      -55
GTC ATC AAC TTC TCC CAA GCA GAG AAA CCC GAA CCC ACC AAC CAG GGG    215
Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly
      -50                      -45                      -40
```

CAG GAT AGC CTG AAG AAA CAT CTA CAC GCA GAA ATC AAA GTT ATT GGG	263
Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile Gly	
-35 -30 -25	
ACT ATC CAG ATC TTG TGT GGC ATG ATG GTA TTG AGC TTG GGG ATC AKT	311
Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile Xaa	
-20 -15 -10 -5	
TTG GCA TCT GCT TCC TTC TCT CCA AAT TTT ACC CAA GTG ACT TCT ACA	359
Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser Thr	
1 5 10	
CTG TTG AAC TCT GCT TAC CCA TTC ATA GGA CCC TTT TTT TTT ATC ATC	407
Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile	
15 20 25	
TCT GGC TCT CTA TCA ATC	425
Ser Gly Ser Leu Ser Ile	
30	

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..347
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 369..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 346..383
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 379..408
id W81335

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..240
id W03593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 239..347
id W03593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 233..389
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..177
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 162..310
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 325..406
id W81261
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..273
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..233
id AA151036
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..430
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 232..389
id AA151036
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..112
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

ATTTTTTTTT CGAGACCGGA AGTGAGTGAT CGAAAGC ATG GCG TCG GTG GTG TTG	55
Met Ala Ser Val Val Leu	
-25 -20	
GCG CTG AGG ACC CGG ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG	103
Ala Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro	
-15 -10 -5	
GCT ACA GCT CTT GCT GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC	151
Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser	
1 5 10	
TCC AAA AAC CTC GGT GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG	199
Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys	
15 20 25	
AAA ATG GAA GGT CAC TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG	247
Lys Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln	
30 35 40 45	
CGC CAT TTC CGC TGG CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG VNT	295
Arg His Phe Arg Trp His Pro Gly Ala His Val Gly Val Gly Lys Xaa	
50 55 60	
AAA TGT CTG TAT GCC CTG GAA GAG GGG ATA GTC CGC TAC ACT AAG GAG	343
Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu	
65 70 75	
GTC TAC GTG CCT CAT CCC AGA AAC ACG GAG GCT GTG GRT CTG ATC ACC	391

Val Tyr Val Pro His Pro Arg Asn Thr Glu Ala Val Xaa Leu Ile Thr
80 85 90

AGG CTG HYC AAG GGT GCT GTG CTC TAC AAG ACT TTT GTC ACG TGG TTC 439
Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys Thr Phe Val Thr Trp Phe
95 100 105

CTG 442
Leu
110

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..347
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 381..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 376..421
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 352..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 346..383
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id AA156841

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 257..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 233..402
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..233
id AA151036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 232..402
id AA151036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..413
id W69555
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..177
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 162..310
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 325..419
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

GGAAGTGAGT GATCGAAAGC ATG GCG TCG GTG GTG TTG GCG CTG AGG ACC CGG      53
      Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg
      -25                      -20                      -15

ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG GCT ACA GCT CTT GCT      101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
      -10                      -5                      1

GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC TCC AAA AAC CTC GGT      149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
      5                      10                      15

GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG AAA ATG GAA GGT CAC      197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
      20                      25                      30

TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG CGC CAT TTC CGC TGG      245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp
      35                      40                      45                      50

CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG AAT AAA TGT CTG TAT GCC      293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala
      55                      60                      65

CTG GAA GAG GGG ATA VWC CGC TAC ACT AAG GAG GTC TAC GTG CCT CAT      341
Leu Glu Glu Gly Ile Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His
      70                      75                      80

CCC AGA AAC ACA GAG GCT GTG GAT CTG ATC ACC AGG CTG CCC AAG GGT      389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly
      85                      90                      95

GCT GTG CTC TAC AAG ACT TTT GTC CAC GTG GTT CCT      425
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro
      100                      105                      110

```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 89..321
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..391
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..50
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 78..313
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 15..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 364..393
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..378
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 62..313
id AA083574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 296..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 312..345
id AA083574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 97..320
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 3..90
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 333..390
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 86..321
id R70112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..94
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 40..87
id R70112
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 111..281
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AIALATVFLIGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```
ATGAGTGGCA CTTAAGCGGG CCATGCCATG CAACCTTGGG CGCTGCCAAC CGTGGGCGAG    60
CTCTGGGTGT GCGGGCGGCC TGGCGCGGCG CTCCGCTGTG TCAGCGTGTT ATG ATG    116
                                     Met Met
CCG TCC CGT ACC AAC CTG GCT ACT GGA ATC CCC AGT AGT AAA GTG AAA    164
Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys Val Lys
-55                      -50                      -45                      -40
TAT TCA AGG CTC TCC AGC ACA GAC GAT GGC TAC ATT GAC CTT CAG TTT    212
Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu Gln Phe
-35                      -30                      -25
AAG AAA ACC CCT CCT AAG ATC CCT TAT AAG GCC ATC GCA CTT GCC ACT    260
Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu Ala Thr
-20                      -15                      -10
GTG CTG TTT TTG ATT GGC GCC TTT CTC ATT ATT ATA GGC TCC CTC CTG    308
Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser Leu Leu
-5                      1                      5
CTG TCA GGC TAC ATC AGC AAA GGG GGG GCA GAC CGG GCC GTT CCA GTG    356
Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val Pro Val
10                      15                      20                      25
CTG ATC ATT GGC ATT CTG GTG TTC CTA CCC GGA TTT TAC CAC    398
Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
30                      35
```

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis

- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 19..351
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 12..344
 id W22200
 est

- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 22..351
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..330
 id R87595
 est

- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 111..287
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 110..286
 id R88526
 est

- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 1..112
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..112
 id R88526
 est

- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 118..331
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 96..309
 id AA031849
 est

- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 28..112
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 49..289
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..53
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 242..286
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
GAAAATTGAA ACTGAGTGGC CCACGATGGG AAGASGGGAA AGCCCAGGGG TACAGGAGGC   60
CTCTGGGTGA AGGCAGAGGC TAACATGAGG TTCGGAGCGA CCTTGGCCGT TGGCCTGACC   120
ATCTTTGTGC TGTCTGTCGT CACTATCATC ATCTGCTTCA CCTGCTCCTG CTGCTGCCTT   180
TACAAGACGT GCCGCCGACC ACGTCCGGTT GTCACCACCA CCACATCCAC CACTGTGGTG   240
C ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT ACC CTG GAC   289
  Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
   -15                -10                -5                1

CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG GGA TGC CAG   337
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
      5                10                15

CAG CAC CCT ACN NAC CAG   355
Gln His Pro Thr Xaa Gln
      20
```

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 49..395
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 12..358
id W22200
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..383
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..332
id R87595
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 141..317
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 110..286
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..142
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..112
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 148..361
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 96..309
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..142
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 141..395
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 49..303
 id T08643
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 93..144
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 2..53
 id T08643
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 272..316
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

AGATTGCTT TCTTTTCTC CAAAAGGGGA GGAAATTGAA ACTGAGTGGC CCACGATGGG      60
AAGAGGGGAA AGCCCAGGGG TACAGGAGGC CTCTGGGTGA AGGCAGAGGC TAACATGGGG      120
TTCGGAGCGA CCTTGGCCGT TGGCCTGACC ATCTTTGTGC TGTCTGTCGT CACTATCATC      180
ATCTGCTTCA CCTGCTCCTG CTGCTGCCTT TACAAGACGT GCCGCCGACC ACGTCCGGTT      240
GTCACCACCA CCACATCCAC CACTGTGGTG C ATG CCC CTT ATC CTC AGC CTC      292
                               Met Pro Leu Ile Leu Ser Leu
                               -15                -10

CAA GTG TGC CGC CCA GCT ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA      340
Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
                               -5                1                5

CCA TGC CGC CTC AGC CAG GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT      388
Pro Cys Arg Leu Ser Gln Gly Cys Gln Gln His Pro Thr Gln Cys Ser
                               10                15                20

ACC CAC CTT GGG      400
Thr His Leu Gly
25

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 152..420
id AA146275
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 152..420
id AA146400
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 199..402

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

ATTTTCAAG ACCGTACTAG GTAGATGGTC AATTAGAGTT CCCAGGGTTT GAAGCCTGTA    60
ACTGCTGCCG CCGCTCAAGC CCTCCAGAGC ATTGCTACGG CTGCTGCCCT TGTACTACTA    120
CCTCCAAATA CGTTCCTTGCT GGTAGTGGCG GCAGCAGGAC CAATTACCTC TTTTGTGCTC    180
TCCCTCGAGA AGCTCCAG ATG GCG TCT TCC GTG GGC AAC GTG GCC GAC AGC    231
          Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser
          -65                      -60

ACA GAA CCA ACG AAA CGT ATG CTT TCC TTC CAA GGG TTA GCT GAG TTG    279
Thr Glu Pro Thr Lys Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu
-55                      -50                      -45

GCA CAT CGA GAA TAT CAG GCA GGA GAT TTT GAG GCA GCB GAG AGA CAC    327
Ala His Arg Glu Tyr Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His
-40                      -35                      -30

TGC ATG CAG CTC TGG AGA CAA GAG CCA GAC AAT ACT GGT GTG CTT TTA    375
Cys Met Gln Leu Trp Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu
-25                      -20                      -15                      -10

TTA CTT TCA TCT ATA CAC TTC CAG TGT CGA AGG CTG GAC AGA TCT GCT    423
Leu Leu Ser Ser Ile His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala
-5                      1                      5

```

CAC TTT AGC ACT CTG GCA
His Phe Ser Thr Leu Ala
10

441

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..218
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 268..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 248..359
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..65
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..47
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 43..228
id AA134712
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..379
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 225..361
id AA134712
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..65
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..47
id AA134712
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 48..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq VILQLQFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

ATTGTAGG	CGCCGGGCAG	CTGAGCTGGT	AGGAGGACCA	GACGGGG	ATG	TTC	GGC	56
					Met	Phe	Gly	
TCC	GCC	CCC	CAG	CGT	CCC	GTG	GCC	104
Ser	Ala	Pro	Gln	Arg	Pro	Val	Ala	
-90				-85			-80	
CTG	TTG	TGG	AAG	CTC	GCG	GGG	TTG	152
Leu	Leu	Trp	Lys	Leu	Ala	Gly	Leu	
-75				-70			-65	
CTG	TCT	GGC	TGT	AGC	ACC	CTG	AGC	200
Leu	Ser	Gly	Cys	Ser	Thr	Leu	Ser	
			-55			-50		
CTG	AAC	CAC	GTA	TTT	GAG	CTG	CAC	248
Leu	Asn	His	Val	Phe	Glu	Leu	His	
			-40			-35		
ACA	GGC	TTT	GTG	GCT	CTG	CCC	TCC	296
Thr	Gly	Phe	Val	Ala	Leu	Pro	Ser	
		-25			-20		-15	
CTT	CAG	CTT	CAG	TTT	CTC	TTC	GAT	344
Leu	Gln	Leu	Gln	Phe	Leu	Phe	Asp	
-10				-5			1	
AAG	CTG	GTC	CAT	GTT	GCT	GGT	CCT	377
Lys	Leu	Val	His	Val	Ala	Gly	Pro	
			10			15		

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 61..312
id N23581
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..77
id N23581
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 310..369
id N23581
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 119..292
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 290..349
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 62..118

id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 13..64
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..331)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 234..518
id HSGT511
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..387)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 177..236
id HSGT511
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 73..314
id W89716
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 314..371
id W89716
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 118..350
id W42358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 350..407
id W42358
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..377
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq LILVGTSKHHVAFG/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```
AGTACATCCG GCGAGTAGCT GGCGGTCCCG GGTGCTGCTG GTTAGTGTGC TCTGAGGGAG   60
GGTCCGAGCC AGCCGCTGTT TTGCCGGAGG AGCCCCTCAG GCCGTAGTAA GCATTAATA   119
ATG TCT TTC ATC TTT GAG TGG ATC TAC AAT GGC TTC AGC AGT GTG CTC   167
Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu
  -85                -80                -75
CAG TTC CTA GGA CTG TAC AAG AAA TCT GGA AAA CTT GTA TTC TTA GGT   215
Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly
  -70                -65                -60                -55
TTG GAT AAT GCA GGC AAA ACC ACT CTT CTT CAC ATG CTC AAA GAT GAC   263
Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
      -50                -45                -40
AGA TTG GGC CAA CAT GTT CCA ACA CTA CAT CCG ACA TCA GAA GAG CTA   311
Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
      -35                -30                -25
ACA ATT GCT GGA ATG ACC TTA CAA CTT TTG ATC TTG GTS GGC ACG AGC   359
Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser
      -20                -15                -10
AAG CAC GTC GCG TTT GGA AAA ATT ATC                               386
Lys His Val Ala Phe Gly Lys Ile Ile
      -5                1
```

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 74..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 78..183
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 176..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 181..266
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..74
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 4..77
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 262..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 263..297
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 78..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 54..297
id W44615
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..61
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..34
id W44615
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..267
id W69940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 57..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..199
id W16769
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 255..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 198..264
id W16769
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..189
id N46069
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..290
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..253
id N46069
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 196..300
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq WYSTVGLLPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
AAAGACGCTC ACGGGCGCGC GGACTATCGG GCGGCTAGGC TCTCTGAGGA GGCTGCCACA   60
GTGAAGCAAC CGTGACAAGT GGTGCCCCGAC CAGGGACCTG AACGAGGAAG GTCTGCCAGA  120
GCAGAGAAAG TGAAACTGAT CAGACGAACT ACGAACCCTT GGACGGGAGA GTCTGCCGGC  180
GGAGAATATA AGGAG ATG GAC AAA CCG TGT GGG TGC CCT CCA GGT GTG TGT   231
      Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys
      -35                -30                -25

GAC CAT GGA ACG GGA GAC CGG AGG GAT CCA TGG TAT TCA ACC GTG GGC   279
Asp His Gly Thr Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly
      -20                -15                -10

CTG TTA CCT CCA GTA CGA GCC ATG AGC CAG CGG AAT CTG AAT   321
```

Leu Leu Pro Pro Val Arg Ala Met Ser Gln Arg Asn Leu Asn
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 161..327
id H07981
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..211
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..155
id H07981
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 193..355
id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 88..188
id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 9..88

id R59645
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 220..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 163..369
id H19239
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 115..220
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 59..164
id H19239
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 2..51
id H19239
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..209
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..178
id AA096397
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 337..371
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 296..330
id AA096397
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 237..266
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 203..232
id AA096397
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 212..345
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 145..278
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 59..121
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 68..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..57
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 25..132
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq ARALAALVPGVTQ/VD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

AGTTTCCGGT TGCCTCCGG AGCC ATG GCG GCG GCA CTG AAG TGT CTA CTG	51
Met Ala Ala Ala Leu Lys Cys Leu Leu	
-35 -30	
ACA TTA GGA AGA TGG TGC CCC GGC CTT GGA GTG GCT CCC CAG GCC CGG	99
Thr Leu Gly Arg Trp Cys Pro Gly Leu Gly Val Ala Pro Gln Ala Arg	
-25 -20 -15	
GCG CTC GCC GCC TTA GTA CCC GGA GTG ACC CAG GTA GAT AAC AAG TCC	147
Ala Leu Ala Ala Leu Val Pro Gly Val Thr Gln Val Asp Asn Lys Ser	
-10 -5 1 5	
GGT TTC CTG CAG AAG AGG CCT CAT CGC CAG CAC CCT GGC ATC CTA AAG	195
Gly Phe Leu Gln Lys Arg Pro His Arg Gln His Pro Gly Ile Leu Lys	
10 15 20	
CTG CCG CAC GTG CGG CTG CCA CAG GCA CTG GCT AAC GGT GCC CAG TTA	243
Leu Pro His Val Arg Leu Pro Gln Ala Leu Ala Asn Gly Ala Gln Leu	
25 30 35	
TTG CTA CTT GGG AGC GCT GGG CCC ACT ATG GAG AAT CAG GTG CAA ACA	291
Leu Leu Leu Gly Ser Ala Gly Pro Thr Met Glu Asn Gln Val Gln Thr	
40 45 50	
CTG ACC AGT TAT CTC TGG AGC AGA CAT TTG CCT GTA GAG CCA GAS GAG	339
Leu Thr Ser Tyr Leu Trp Ser Arg His Leu Pro Val Glu Pro Xaa Glu	
55 60 65	

TTG CAA AGA CGG GCT ARG CAT CTT GAG AAA AAA TTC CTG GAA AAC CCA 387
Leu Gln Arg Arg Ala Xaa His Leu Glu Lys Lys Phe Leu Glu Asn Pro
70 75 80 85
GAC TTA TCT CAG ACA GAG GAG AAA CTT CGT GGA GCA GGG 426
Asp Leu Ser Gln Thr Glu Glu Lys Leu Arg Gly Ala Gly
90 95

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 160..350
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 24..107
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 100..149
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 13..159
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 170..268
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 281..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 268..363
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 22..147
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..267
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 200..283
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..361
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 325..381
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 140..189
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 129..321
id N40684
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 56..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..118
id N40684
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 267..399
id AA005400
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 120..235
id AA005400
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 31..336
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq TVMSALSVAPSKA/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGTGTCTT GCGCGTGGAT CCGAGCGACC ATG GTG GCC CGG GTG TGG TCG CTG	54
Met Val Ala Arg Val Trp Ser Leu	
-100 -95	
ATG AGG TTC CTC ATC AAG GGA AGT GTG GCT GGG GGC GCC GTC TAC CTG	102
Met Arg Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu	
-90 -85 -80	
GTG TAC GAC CAG GAG CTG CTG GGG CCC AGC GAC AAG AGC CAG GCA GCC	150
Val Tyr Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala	
-75 -70 -65	
CTA CAG AAG GCT GGG GAG GTG GTC CCC CCC GCC ATG NAC CAG TTC AGC	198
Leu Gln Lys Ala Gly Glu Val Val Pro Pro Ala Met Xaa Gln Phe Ser	
-60 -55 -50	
CAG TAC GTG TGT CAG CAG ACA GGC CTG CAG ATA CCC CAG CTC CCA GCC	246
Gln Tyr Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala	
-45 -40 -35	
CCT CCA AAG ATT TAC TTT CCC ATC CGT GAC TCC TGG AVT GCA GGC ATC	294
Pro Pro Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Xaa Ala Gly Ile	
-30 -25 -20 -15	

ATG ACG GTG ATG TCA GCT CTG TCG GTG GCC CCC TCC AAG GCC CGC GAG 342
Met Thr Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu
-10 -5 1

TAC TCC AAG GAG GGC TGG GAG TAT GTG AAG GCG CTT GGG 381
Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala Leu Gly
5 10 15

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..204
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 185..271
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 289..337
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..338
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 11..341
id T93683
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..295
id AA015679
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 398..445
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AGTTTGTAGC GGACAACATG GCGGCCTTCA TGCTGGGCTC GCTGCTGCGG ACGTTCAAGC   60
AGATGGTTCC TTCATCAGCT TCAGGCCAAG TTCGAAGTCA CTATGTAGAC TGGAGAATGT   120
GGCGCGATGT GAAGAGACGA AAAATGGCCT ATGAATACGC AGATGAGAGG CTACGTATTA   180
ATTCACCTCAG GAAGAATACC ATTTTGCCAA AAATTCTTCA GGATGTGGCT GATGAAGAAA   240
TTGCTDHCCT CCCCCGGGAT AGCTGTCCTG TTAGAATCAG AAATCGGTGT GTTATGACGT   300
CCCGTCCGCG TGGTGTGAAG CGGCGCTGGA GGCTTAGTCG TATAGTCTTC CGTCACTTAG   360
CTGACCATGG GCAACTTTCT GGGATCCAGC GAGCGAC ATG GTA AAT GAG CTC CAG   415
                               Met Val Asn Glu Leu Gln
                               -15

AAC CTA TNG AGC TTG CAG GGA AGC CAA GCT TGC AGT TCC AGC AAG CAA   463
Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala Cys Ser Ser Ser Lys Gln
-10          -5          1          5

AGA TTT   469
Arg Phe
```

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 102..220
id T30988
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..92
id T30988
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..225
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 110..213
id T30974
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 13..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..100
id T30974
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 84..202
id HSCOCC031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..74
id HSCOCC031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 84..202
id HSCOCD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..74
id HSC0CD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..117
id R56565
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 80..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FFFSIQPFLLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```
AACACACTCC CTCTCTCTCT CTTTITAGCA GCAACATACA AGCCGGCCAT ATTAGAGAGA 60
TGGAAATAAA GCTTCCTTA ATG TTG TAT ATG TCT TTG AAG TAC ATC CGT GCA 112
      Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala
                        -20                      -15
TTT TTT TTT AGC ATC CAA CCA TTC CTC CCT TGT AGT TCT CSC CCC CTC 160
Phe Phe Phe Ser Ile Gln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu
      -10                      -5                      1
AAA TCA CCC TCT CCC GTA GCC CAC CCG ACT AAC ATC TCA GTC TCT GAA 208
Lys Ser Pro Ser Pro Val Ala His Pro Thr Asn Ile Ser Val Ser Glu
      5                      10                      15
AAT GCA CAG AGA TGC CTN NCT ACC TCG CCC TGG 241
Asn Ala Gln Arg Cys Leu Xaa Thr Ser Pro Trp
      20                      25                      30
```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 167..398
id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..116
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 38..102
id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 99..155
id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 202..399
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..116
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 73..137
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..259
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 213..292

id W25483
est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 111..168
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 144..201
 id W25483
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 52..100
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 85..133
 id W25483
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 180..278
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 194..292
 id C17967
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 52..111
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 65..124
 id C17967
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 111..168
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 125..182
 id C17967
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 280..341
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 293..354
 id C17967
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 180..411
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 273..504
id AA032534
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 107..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 200..261
id AA032534
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 110..346
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq WVIVLTSWITIFQ/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACATAACTGA AAGTAGCTAA GGCACCCCAG CCGGAGGAAG TGAGCTCTCC TGGGTCAAGG      60
CTTGGGTCTT GCCCCGCAGA CCCTTGGGAC GACCCGGCCC CAGCGCAST ATG AAC CTG      118
                                     Met Asn Leu
GAG CGA GTG TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC      166
Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr
-75                               -70                               -65
CTG GGG GGG TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC      214
Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe
-60                               -55                               -50                               -45
TGG TTC TTC CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC      262
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser
-40                               -35                               -30
CAA ATC AAA GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG      310
Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
-25                               -20                               -15
GTG ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC      358
Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
-10                               -5                               1
CGC TGG GGT GCC CTH GGG GAC TAS CTC TCC TTC ACC ATA CCC CTG GGC      406
Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile Pro Leu Gly
5                               10                               15                               20
ACC CCT GAC AAC TTC TGC ACA TAC      430
Thr Pro Asp Asn Phe Cys Thr Tyr
25

```

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 167..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 144..359
 id T27537
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 27..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 2..137
 id T27537
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 162..380
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 89..307
 id AA057488
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 75..172
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 1..98
 id AA057488
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 175..381
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 72..278
 id H10316
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 105..174
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 1..70
id H10316
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 162..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 60..283
id T33282
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..162
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..59
id T33282
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 174..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 65..287
id R14076
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..62
id R14076
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 122..331
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

AATTGCCTGC CTGAGTCACG TGTCAGGGGG AAGCTGGAAG GCGTCGTTCT CCTTTCCCAG 60

CTCTCCTGCC TGTCGCCCAT GTTTTCAGGC CGGGTCTGGC TTGGTCTTCC CCCGTAAGRA 120

A ATG GCC GGG GAG CTC CAG GGG ACC CAG GCG CCG TCG CTT CGD GGA SCT 169
Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
-70 -65 -60 -55

GGG CTG ACC AGC CAG GAC AGC GGG GTA AAC CCG AAC AAT TCT GYG CGA 217
Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg

-50	-45	-40	
GGT AGG GAG GCC ATG GCG TCC GGC AGT AAC TGG CTC TCC GGG GTG AAT			265
Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn			
-35	-30	-25	
GTC GTG CTG GTG ATG GCC TAC GGG AGC CTG GTG TTT GTA CTG CTA TTT			313
Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe			
-20	-15	-10	
ATT TTT GTG AAG AGG CAA ATC ATG CGC TTT GCA ATG AAA TCT CGA AGG			361
Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg			
-5	1	5	10
GGA CCT CAT GTC CCT GTR GGR NCA CAA TGC CCC CAA KGT TGC TAC AAC			409
Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn			
15	20	25	
TAT CTG TAT			418
Tyr Leu Tyr			

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 91..360
id C17648
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..104
id C17648
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 93..262

id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 261..363
id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..56
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..58
id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 59..89
id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 95..252
id W00492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..60
id W00492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 255..313
id W00492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..342
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 311..345
id W00492
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..362
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 64..366
id N29017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 8..70
id N29017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..359
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 121..386
id N31560
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 116..283
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```
AAACGGAGGC AGGTTGGAGC CGCTGCCGTC GCCATGACCC GCGGTAACCA GCGTGAGCTC   60
GCCCGCCAGA AGAATATGAA AAAGCAGAGC GACTCGGTTA AGGGAPAGCG CCGAG ATG   118
                                         Met
ACG GGC TTT CTG CTG CCG CCC GCA AGC AGA GGG ACT CGG AGA TCA TGC   166
Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser Cys
-55                               -50                               -45                               -40
AGC AGA AGC AGA AAA AGG CAA ACG AGA AGA AGG AGG AAC CCA AGT AGC   214
Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser Ser
-35                               -30                               -25
TTT GTG GCT TCG TGT CCA ACC CTC TTG CCC TTC GCC TGT GTG CCT GGA   262
Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro Gly
-20                               -15                               -10
GCC AGT CCC ACC ACG CTC GCG TTT CCT CCT GTA GTG CTC ACA GGT CCC   310
Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly Pro
```

-5

1

5

AGC ACC GAT GGC ATT CCC TTT GCC CTG AGT CTG CAG MGG GTC CCT TTT 358
Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro Phe
10 15 20 25
GTG 361
Val

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..459)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 565..794
id HS278357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..205)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 818..1021
id HS278357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 310..337
id AA052404
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 62..175
id H75454
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 30..94
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..65
 id H75454
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 230..307
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AACTTCCAAG TTGTAGTGTT GTTGTTTTCA GCCTGCTGCT GCTGCTGCTA TTGCGGCTAG   60
GGGAACCGTC GTGGGAAGG ATGGTGTGCG AAAAATGTGA AAAGAACTT GGTACTGTTA   120
TCACTCCAGA TACATGGAAA GATGGTGCTA GGAATACCAC AGAAAGTGGT GGAAGAAAGC   180
TGAATGAAAA TAAAGCTTTG RCTTCAAAAA AAGCCAGAAT TGAWCCATA ATG GAA GAA   238
                                     Met Glu Glu
                                     -25

WTA AGT KCT CCA CTT GTA GAA TTT GTA AAA GTT TTG TGC ACC AAC CAG   286
Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
      -20                      -15                      -10

GTT CTC ATT ACT GCC AGG GCT GTG CCT ACA AAA AAG GCA TCT GTG CGA   334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
      -5                      1                      5

TGT GTG GMA AAA AGG TTT TGG ATA CCA AAA ACT ACA AGC AAA CAT CTG   382
Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
    10                      15                      20                      25

TCT AGA TGT ATT GAT GGA ATT TCT GGC TTT CTA AAT GAT TTT ACT TTC   430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
      30                      35                      40

TGC CTT GAA TTT TCA AGG CAT AGA TGT   457
Cys Leu Glu Phe Ser Arg His Arg Cys
      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 119..361
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..120
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 124..260
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..125
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 251..309
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 101..343
id N40141
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 24..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..102
id N40141
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 122..326
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..123
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..367)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 112..354
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(73..125)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 353..405
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LXXVVAFVAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```
ATTCTTTCTT CGCCAGGCTC TCTGCTGACT CAAGTTCTTC AGTTCACGAT CTTCTAGTTC 60
CAGCGATGAG TGCACGAGTG AGATCAAGAT CCAGAGGAAG AGGAG ATG GTC AGG AGG 117
                                     Met Val Arg Arg
                                     -15

CTM MCG AWT GTG GTT GCA TTC GTG GCT CCC GGT GAA TCT CAG CAA GAG 165
Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu Ser Gln Gln Glu
```

-10

-5

1

GAA CCA CCA ACT GAC AAT CAG GAT ATT GAA CCT GGA CAA GAG AGA GAA	213
Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg Glu	
5 10 15	
GGA ACA CCT CCG ATC GAA GAA CGT AAA GTA GAA GGT GAT TGC CAG GAA	261
Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln Glu	
20 25 30 35	
ATG GAT CTG GAA AAG ACT CGG AGT GAG CGT GGA GAT GGC TCT GAT GTA	309
Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp Val	
40 45 50	
AAA GAG AAG ACT CCA CCT AAT CVT AAG CAT GCT AAG ACT AAA GAA GCA	357
Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys Thr Lys Glu Ala	
55 60 65	
GGA GAT GGG CCA TTG	372
Gly Asp Gly Pro Leu	
70	

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 299..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 273..433
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 133..236
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..159
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..136
id AA100750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..347
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 355..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 348..395
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 400..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 394..423
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 5..245
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 239..337
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 244..342
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq PIVRLLSCPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TKTTTTTTAG CA ATG GCG GTT CCC GGC GTG GGG CTC TTG ACC CGT TTG AAC 51
Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn

	-35	-30	-25	
CTG TGT GCC CGG AGA AGA ACT CGA GTC CAG CGG CCT ATC GTC AGG CTT				99
Leu Cys Ala Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu	-20	-15	-10	
TTG AGT TGC CCA GGA ACT GTG GCC AAA GAC CTT AGG AGA GAC GAG CAG				147
Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln	-5	1	5	
CCT TCA GGG AGC GTG GAG ACA GGC TTT GAA GAC AAG ATT CCC AAA AGG				195
Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg	10	15	20	
AGA TTC TCG GAG ATG CAA AAT GAA AGA CGA GAA CAG GCA CAG CGG ACT				243
Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr	25	30	35	40
GTT TTA ATA CAT TGC CCA GAG AAA ATC AGT GAA AAC AAG TTT CKK AAA				291
Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys	45	50	55	
TAT TTA TCC CAA TTT GGA CCT ATT AAT AAT CAT TTC TTC TAT GAA AGC				339
Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser	60	65	70	
TTT GGT CTC TAT GCT GTC GTA GAA TTT TGC CAA AAG GAA AGC ATA GGT				387
Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly	75	80	85	
TCA CTG CAG AAT GGG ACT CAT ACT CCA AGC ACG GCC ATG GAG ACT GCA				435
Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala	90	95	100	
ATT CCA TTC AGA TCA CGT TCT TCA				459
Ile Pro Phe Arg Ser Arg Ser Ser	105	110		

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 43..253
id AA017309

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 93..124
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 28..59
 id AA017309
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(126..250)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..125
 id T52392
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 21..200
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.8
 seq LVILSLKSQTLDA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AGTAAGTCCC CCCGCCTCGC ATG ATG GCT GCG GTG CCG CCG GGC CTG GAG CCG      53
      Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
      -60              -55              -50

TGG AAC CGT GTG AGA ATC CCT AAG GCG GGG AAC CGC AGC GCA GTG ACA      101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
      -45              -40              -35

GTG CAG AAC CCC GGC GCG GCC CTT GAC CTT TGC ATT GCA GGT GTA ATT      149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
      -30              -25              -20

AAA GAA TGC CAT CTC GTC ATA CTG TCG CTG AAG AGC CAA ACC TTA GAT      197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
      -15              -10              -5

GCA GAA ACA GAT GTG TTA TGT GCA GTC CTT TAC AGC AAT CAC AAC AGA      245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
      1              5              10              15

ATG GGC CGC CAC AAA CCC CAT TTG GCC CTC AAA CAG GTT GAG CAA TGT      293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Gln Gln Cys
      20              25              30

TTA AAG CGT TTG ARA AAC ATG AAT TTG GAG GGC GGG                        329
Leu Lys Arg Leu Xaa Asn Met Asn Leu Glu Gly Gly
      35              40

```

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..347
id AA023764
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 145..384
id C03036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..80
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 2..71
id C03036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..193
id R08519
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 193..263
id R08519
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..109

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.8
 seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA	49
Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly	
-30 -25	
GAC TCA GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT	97
Asp Ser Gly Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn	
-20 -15 -10 -5	
CAA GTG CTG GGA AAT CCA TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC	145
Gln Val Leu Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val	
1 5 10	
AGA GTK CAT GAT TAC AAA GAA GGA ACC CCA GAA GAG AAG ACC TAC TAC	193
Arg Val His Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr	
15 20 25	
ATA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC AGC GTG	241
Ile Glu Leu Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val	
30 35 40	
AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATW NYC	289
Lys Ser Thr Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa	
45 50 55 60	
GTA CAC GAC TTA ACV SAT GGG AAG TCC TCC CAA AAM TTG CGN CGT TGG	337
Val His Asp Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp	
65 70 75	
TCA TTG GAA GCT CTC AAC AGG GAT TTG GTG CCA ACT GGA GTC TTG GTG	385
Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val	
30 85 90	

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 12..219

id R19497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 219..253
id R19497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..185
id H75597
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 184..218
id H75597
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..173
id H93398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 178..212
id H93398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..173
id HUM030E11B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..127
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 118..244
id AA280273
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPsRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
GCGTCCGCGC CATCAGGCCC GAGATAGCGG CGAGGTCCGC TTTCAGTGT ATG GTT TTC    58
                                   Met Val Phe
                                   -30

CCT GCC AAA CGG TTC TGC TTG GTG CCA TCC ATG GAG GGC GTG CGC TGG    106
Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly Val Arg Trp
      -25                -20                -15

GCC TTT TCC TGC GGC ACT TGG CTG CCG AGC CGA GCC GAA TGG CTG CTK    154
Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu Trp Leu Leu
      -10                -5                1

RCA GTG CGA TCG ATT CAG CCC GAG GAG AAG GAG CGC ATT GGC CAG TTC    202
Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile Gly Gln Phe
      5                10                15                20

GTC TTT GCC CGG GAC GCT AAG GCA GCC ATG GCT GGT CGT CTG ATG ATA    250
Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg Leu Met Ile
                25                30                35

AGG AAA TTA GTT GCA GAG AAT CGA                                274
Arg Lys Leu Val Ala Glu Asn Arg
      40
```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrrenals

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 90..208
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 105..223

id HSC13B041
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 18..115
id HSC13B041
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 90..208
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 71..189
id T08849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..81
id T08849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..101
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..83
id H88132
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 90..158
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 71..139
id H88132
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..208
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 140..190
id H88132
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..208
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 92..189
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..110
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..92
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 141..179
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ACTTTCCTCAA G ATG GCG TCG AAG ATA GGT TCG AGA CGG TGG ATG TTG CAG	50
Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln	
-25 -20 -15	
CTG ATC ATG CAG TTG GGT TCG GTG CTG CTC ACA CGC TGC CCC TTT TGG	98
Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp	
-10 -5 1	
GGC TGC TTC AGC CAG CTC ATG CTG TAC GCT GAG AGG GCT GAG GCA CGC	146
Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg	
5 10 15	
CGG AAG CCC GAC ATC CCA GTG CCT TAC CTG TAT TTC GAC ATG GGG GCA	194
Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala	
20 25 30 35	
GCC GTG CTG TGC GCG CGG	212
Ala Val Leu Cys Ala Arg	
40	

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..272
id W52056
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAGAACTGCG TCTCGCGACC CAGGCGCGGG TTCCCGGAGG ACAGCCACCA AGCGATGCTG      60
CCGCCGCCGT TTCCTGATTG GTTGTGGGTG GCTACCTCTT CGTTCTGATT GGCCGCTAGT     120
GAGCAAG ATG CTG AGC AAG GGT CTG AAG CGG AAA CGG GAG GAG GAG GAG      169
    Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
        -30                -25                -20

GAG AAG GAA CCT CTG GCA GTC GAC TCC TGG TGG CTA GAT CCT GGC CAC      217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
    -15                -10                -5

GCA GCG GTG GCA CAG GCA CCC CCG GCC GTG GCC TCT AGC TCC CTC TTT      265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
    1                5                10                15

GAC CTC TCA GTG CTC AAG CTC CAC CAC AGC CGC GGG                        301
Asp Leu Ser Val Leu Lys Leu His His Ser Arg Gly
        20                25

```

(2) INFORMATION FOR SEQ ID NO: 231:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 88..277
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 36..89
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 345..379
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..36
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 313..344
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..316
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 279..312
id W02951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 81..293
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 292..363
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 291..367
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 28..81
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 93..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 79..367
id R91018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..80
id R91018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 13..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..81
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 291..366
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 282..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq SLAAPALTLHGHWG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

AAGGAACGAG ATGGCGGTTT TCTGGAGGCT GAGTGCCGTT TGGGGTGCCC TAGGAGGCCG 60
AGCTCTGTTG CTTTGAATCT CAGTGGTCAG AMCTTGCTCA TATCTCAGCA TTTCTTCAGG 120
ACCGACCTAT CCCAGAAATGG TGTGGAGTGC AGCACATACA CTTGTACCG AGCCACCATT 180
CTGGCTCCAA GGCTGCATCT CTCCACTGGA CTAGCGAGAG GGTGTGTCAGT GTTTTGCTCC 240

TGGGTCGTGCT TCCGGCTGCT TATTGAATC CTTGCTCTGC G ATG GAC TAT TCC CTG 296
Met Asp Tyr Ser Leu
-15

GCT GCA GCC CTC ACT CTT CAT GGT CAC TGG GGC CTT GGA CAA GTT GTT 344
Ala Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val
-10 -5 1 5

ACT GAC TAT GTT CAT GGG GAT GCC TTG CAG AAA GCT 380
Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala
10 15

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 123..338
id HUM09CD043
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..134
id HUM08CD043
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 339..399
id HUM08CD043
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 407..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 397..435
id HUM080D04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 127..263
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..133
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 263..338
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 339..378
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 374..403
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 123..338
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..143

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..134
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..397
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 339..388
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 407..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 396..426
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..299
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 135..296
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..141
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 292..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 290..346
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 402..441
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 407..446
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 138..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 94..282
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 44..143
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..100
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 348..408
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 306..366
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 181..396
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq LSLXASYIFGISG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```

AGTTTTCAGG ARATTGGAA GCTGCCGCG TAGTTGGAGT CTAAGGACTC GTGACAATCT   60
TCGGGTGCCC TTCGAGAGAA AAGGGGAGGA TGCCACTGGA GTCATCCTCT TCAATGCCAC   120
TATCCTTCCC ATCTBYBYTD RCCCTCRGTA CCACACAATA CTAACCCTTC CCCTNCTCTG   180
ATG TCT TAC ATC ACC TCC CAG GAG ATG AAG TGT ATT CTT CAC TGG TTT   228
Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
   -70               -65               -60

GCC AAT TGG TCA GGT CCC CAG CGT GAA CGT TTC CTA GAG GAC CTG GTA   276
Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
   -55               -50               -45

GCT AAG GCA GTG CCA GAA AAA TTA CAA CCA HTG CTG GAT AGT CTG GAG   324
Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
   -40               -35               -30               -25

CAG CTT AGT GTG TCT GGG GCA GAC GAC CAC CTT CTA TCT TTG WGT GCC   372
Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
   -20               -15               -10

AGC TAC ATC TTT GGG ATC AGT GGT TTC GAG GCT GGG GCT GAG CAG GAG   420
Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
   -5               1               5

```

CGC AAT GAA TTT GTC AGA CAG TCG
Arg Asn Glu Phe Val Arg Gln Ser
10 15

444

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 6..366
id W31798
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..353
id AA056667
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 4..342
id AA131958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..334
id H10262
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..406
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..330
id W95790
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 200..427
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

AAGACGAGGT CATGAATCAT GTGACGGTGG CTTGAGGAGG AACCTGTCTT TAAAGCTGTC   60
CCTGAAGTGA CAGCGGAGAG AACCAGGCAG CCCAGAAACC CCAGGCGTGG AGATTGATCC   120
TGCGAGAGAA GGGGGTTCAT CATGGCGGAT GACCTAAAGC GATTCTTGTA TAAAAAGTTA   180
CCAAGTGTG AAGGGCTCC ATG CCA TTG TTG TGT CAG ATA GAG ATG GAG TAC   232
      Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
      -75                               -70

CTG TTA TTA AAG TGG CAA ATG ACA ATG CTC CAG AGC ATG CTT TGC GAC   280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65                               -60                               -55                               -50

CTG GTT TCT TAT CCA CTT TTG CCC TTG CAA CAG ACC AAG GAA GCA AAC   328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
      -45                               -40                               -35

TTG GAC TTT CCA AAA ATA AAA GTA TCA TCT GTT ACT ATA ACA CCT ACC   376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
      -30                               -25                               -20

AGG TGG TTC MAT TTA ATC GTT TAC CTT TGG GTG GTG AGT TTC ATA GCC   424
Arg Trp Phe Xaa Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
      -15                               -10                               -5

AGC AGC AGT   433
Ser Ser Ser
1

```

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 39..179
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 161..261
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..219
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 22..224
id W07092
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 140..377
id W72958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 18..255
id W24219
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 16..253
id AA040714
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq SVMGVCLLPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAGGACCCA GAAGTAGGGT TTTGGCCTAG GTAACGGGGC AGAG ATG TGG TTC GAG      56
                                   Met Trp Phe Glu
                                   -20

ATT CTC CCC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT CCA GGA      104
Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile Pro Gly
      -15                      -10                      -5

CTG GCT ACT GCG TAC ATC CAC ARG TTC ACT AAC CGG GGC AAG GAA AAA      152
Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg Gly Lys Glu Lys
      1                      5                      10

AGG GTT GCT CAT TTT GGG TAT CAC TGG AGT CTG ATG GAA AGA GAT AGG      200
Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met Glu Arg Asp Arg
      15                      20                      25                      30

CGC ATC TCT GGA GTT GAT CGT TAC TAT GTG TCA AAG GGT CCA GGG      245
Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys Gly Pro Gly
      35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 162..309
id AA017973
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 181..328
id AA021972
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 181..328
id AA013987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 168..315
id AA014054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 184..331
id W80073
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 205..342
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```
AGTTTAGCGA CCGGACCCGA AACGGGGAAG TTGTCTTG TGAGAGGTT AGTAAAGCAG    60
CGCGCGCGTC ACCAGAGTCG TTTCTCTTCG GAGTCTTAGG TGATCGAGGG TGTGCCCAGG   120
GGGCGGACTT GTTGCGCCT CCCGTTCCCT CCCAATTTC AAACGTGTCA CCCC GGCGCC    180
GACGGCCCTG TGCAGGGGAA GCAG ATG GAG TTC AAG CTG GAG GCT CAT CGC      231
                Met Glu Phe Lys Leu Glu Ala His Arg
                -45                      -40

ATC GTC AGC ATC TCT CTG GGC AAG ATC TAC AAC TCG CGG GTC CAG CGC      279
Ile Val Ser Ile Ser Leu Gly Lys Ile Tyr Asn Ser Arg Val Gln Arg
    -35                -30                -25

GGC GGC ATC AAG CTG CAT AAG AAC CTC CTG GTC TCG CTG GTG CTG CGC      327
Gly Gly Ile Lys Leu His Lys Asn Leu Leu Val Ser Leu Val Leu Arg
    -20                -15                -10

ASG CCC GCC AAG TCT ACC CGA GCG GGG                                354
Xaa Pro Ala Lys Ser Thr Arg Ala Gly
    -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..179
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 179..333
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..363
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..285
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 338..381
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 307..336

id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 27..337
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 347..382
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..216
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 271..332
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 216..278
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 332..376
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..368
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..310
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 370..414
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 311..355
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IASGLGLXLCWT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCTAGCCC CGCCCCAGGC GAGGGCGCCG CACCCACACC GCGCTGCGCA GTTTTGTCT 60
GCTCCAGCTG TTCGAAGGTG ATCCAGACGC AAG ATG GCT GTC CTC TCT AAG GAA 114
                               Met Ala Val Leu Ser Lys Glu
                               -95

TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC 162
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
-90                               -85                               -80                               -75

CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG 210
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
                               -70                               -65                               -60

TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC 258
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
                               -55                               -50                               -45

TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CSC TTC 306
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Xaa Phe
                               -40                               -35                               -30

TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT 354
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
                               -25                               -20                               -15

GGC CTG GGC TTG DCN CTG GAT TGT TGG ACG AGT TCT TTA TGC TTA TGG 402
Gly Leu Gly Leu Xaa Leu Asp Cys Trp Thr Ser Ser Leu Cys Leu Trp
-10                               -5                               1                               5

CTA TTA CAC GGG CCG GGG 420
Leu Leu His Gly Pro Gly
                               10

```

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..227
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..200
id AA074804
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 265..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 238..283
id AA074804
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..263
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 201..237
id AA074804
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 352..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 328..361
id AA074804
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(259..408)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 123..272
id N93600
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(85..207)

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
 region 325..447
 id N93600
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(202..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
 region 117..323
 id AA074748
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(116..153)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
 region 375..412
 id AA074748
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(167..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
 region 324..359
 id AA074748
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(258..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
 region 123..273
 id N93603
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(208..251)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
 region 280..323
 id N93603
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(163..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
 region 329..368
 id N93603
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(90..125)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 411..446
 id N93603
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 272..397
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq RIPS LPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

AAAAGGAAAG AGGTYSGGAG CGCTCGCGAG ATCTCGGACC ACCCAACCTG AAAGGTGCTT   60
AGGAAGTTGA AAGGCCCAGA GGAGGCCTCC GGGCAAATGG CCGGAGCTGG ACCGACCATG  120
CTGCTACGAG AAGAGAATGG CTGTTGCAGT CGGCGTCAGA GCAGCTCCAG TGCCGGGGAT  180
TCGGACGGAG AGCGCGAGGA CTCGGCGGCT GAGCGCGCCC GACAGCAGCT AGAGGCGCTG  240
CTCAACAAGA CTATGCGCAT TCGCATGACA G ATG GAC GGA CAC TGG TCG GCT      292
                               Met Asp Gly His Trp Ser Ala
                               -40

GCT TTC TCT GCA CTG ACC GTG ACT GCA ATG TCA TCC TGG GCT CGG CGC      340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                -30                -25                -20

AGG AGT TCC TCA AGC CGT CGG ATT CCT TCT CTG CCG GGG AGC CCC GTG      388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
          -15                -10                -5

TGC TGG GCC TGG CCA TGG                                          406
Cys Trp Ala Trp Pro Trp
      1
  
```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (E) TISSUE TYPE: Liver

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 56..207

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 20..171
id N41898
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 38..176
id H69272
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLLRRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```
ACTTGACAGG CAGGGAGGGC TAGGCTGTGC ATCCCTCCGC TCGCATTGCA GGGAG ATG      58
                                         Met
GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT GTC ATC TCC AGG      106
Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser Arg
-15                      -10                      -5                      1
AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC AGA GCC CTG CAG      154
Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu Gln
                      5                      10                      15
ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA CCC AAC CCA GCC      202
Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro Ala
                20                      25                      30
CGG ACG
Arg Thr
35
```

208

(2) INFORMATION FOR SEQ ID NO: 239:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 103..322
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 4..115
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..398
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 336..377
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..337
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..391
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..385
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..134
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..128
id AA054941
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 191..283
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..277
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 117..184
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 361..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 360..397
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 97..316
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..108
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 330..371
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(153..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 108..255
id H72704
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(291..343)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 64..116

id H72704
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(101..151)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 259..309
id H72704
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(357..398)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 9..50
id H72704
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 311..385
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq FLLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
AGACGTGTTC TTCCGGTGGC GGASGGCGGA TTAGCCTTCG CGGGGCAAAA TGGAGCTCGA    60
GGCCATGAGC AGATATACCA GCCCAGTGAA CCCAGCTGTC TTCCCCCATC TGACCGTGGT    120
GCTTTTGGCC ATTGGCATGT TCTTCACCGC CTGGTTCTTC GTTTACGAGG TCACCTCTAC    180
CRAGTACACT CGTGATATCT ATAAAGAGCT CCTCATCTCC TTAGTGGCCT CACTCTTCAT    240
GGGCTTTGGA GTCCTCTTCC TGCTGCTCTG GGTGCGCATC TACGTGTGAG CACCCCAAGGG    300
TAACAACCAG ATG GCT TCA CTG AAA CCT GCT TTT GTA AAT TAC TTT TTT    349
      Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe
      -25                -20                -15

TTA CTG TTG CTG GAA GTG TCC CAC CTG CTG CTC ATA ATA AAT GCA GAA    397
Leu Leu Leu Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu
      -10                -5                1

GGG                                          400
Gly
5
```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..396

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 202..372
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 27..162

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 158..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 213..292
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 157..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..182
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 293..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 167..337
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155

id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 226..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 177..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 156..386
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

AAAAACGTCC ATRACTGAAA GTAGCTAAGG CACCCCAGCC GGAGGAAGTG AGCTCTCCTG      60
GGGCGTGGTT GTTCGTGATC CTTCATCTG TTAAGTAGGG TCAAGGCTTG GGTCTTGCCC      120
CGCAGACCCCT TGGGACGACC CGGCCCCAGC GCAAT ATG AAC CTG GAG CGA GTG      173
                               Met Asn Leu Glu Arg Val
                               -75

TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC CTG GGG GGG      221
Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr Leu Gly Gly
-70                               -65                               -60

TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC TGG TTC TTC      269
Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe Trp Phe Phe
-55                               -50                               -45                               -40

CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC CAA ATC AAA      317
Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser Gln Ile Lys
-35                               -30                               -25

GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG GTG ATA GTG      365
Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp Val Ile Val
-20                               -15                               -10

CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC      395
Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
-5
1

```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 170..205
id AA090974
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```
ATTTTTTCT TGCTCGTGGG CTCGGACGAG TACGGAGCGC CTGCAGGGAC AGCCTGGATA    60
AAGGCTCACT TG ATG GCT CAG TTG GGA GCA GTT GTG GCT GTG GCT TCC AGT    111
           Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser
           -20                      -15                      -10

TTC TTT TGT GCA TCT CTC TTC TCA GCT GTG CAC AAG ATA GAA GAG GGA    159
Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly
           -5                      1                      5

CAT ATT GGG GTA TAT TAC AGA GGC GGT GTG                                189
His Ile Gly Val Tyr Tyr Arg Gly Gly Val
           10                      15
```

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 16..262
id AA044042
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..33
id AA044042
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 6..239
id AA127902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..216
id AA056679
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(104..308)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 246..450
id W93399
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..184
id H39528
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 122..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```
GCGAAGGTTG TCGGGATCCG CGGCAGCAGC GGCTGCTTGA GATCTGTTTC TGGGGCCTCT    60
GCGGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGC GCAG GTACACTGAT GCTGAAGTAC    120
T ATG AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT TTT ATG    169
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25          -20          -15          -10

GTC CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC    217
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5          1          5

AGC CCT GTT TTC CAA ATA CCT AAA AAC GAC GAC ATT CCT GAG CAA GAT    265
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
          10          15          20

ACT CTG GGA CTT TCA AAT CTT CAG AAG AGC CAA ATC CAG GGG ATA CTG    313
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
          25          30          35
```

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 33..282
id AA088487
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 341..409
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VFCLLISIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

AGTCGTTGCC ATSGATCCTG GGGACGACTG GCTGGTGGAA TCCTTGCCTG TGTAATCGT    60
ACCAGGATTT CTATGCATTC GACCTGTCAG GAGCCACTCG AGTCCTTGAA TGGATTGATG   120
ACAAAGGAGT CTTTGTGCT GGCTATGAAA GCCTGAAAAA GAATGAAATT CTTCATCTGA   180
AATTACCTCT CAGACTTTCT GTAAAGGAAA ACAAGGGCTT ATTCCCAGAA AGAGATTTCA   240
AAGTGCGCCA TGGAGGATTT TCAGACAGGT CTATCTTTGA TCTAAAGCAT GTGCCACATA   300
CCAGGTATGG TCAATTTTGT GATCCAGCCA TCCACACAGG ATG GGA TGG GAT GGC    355
                                         Met Gly Trp Asp Gly
                                         -20

TGC AAA TGC CTG GGG GTA TTC TGC CTC CTC ATC TCC ATT CCC ACC CCC    403
Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile Ser Ile Pro Thr Pro
      -15                      -10                      -5

TCA GCA CAC CTG                                          415
Ser Ala His Leu
      1

```

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..451
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 122..417
id AA085629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 14..114
id AA085629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..259
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 134..237
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 29..126
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 254..294
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 15..112
id H35088
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 156..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 63..252
id HUML11153
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..365
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq ILAHLRLGLIPIHA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```
AGAGATTGAA G ATG GCG GCT TCT CAG GCG GTG GAG GAA ATG CGG ACC GCG      50
      Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala
              -115                      -110

TGG TTC TGG GGG AGT TTG GGG TTC GCA ATG TCC ATA CTA CTG ACT TTC      98
Trp Phe Trp Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe
-105              -100                      -95                      -90

CCG GTA ACT ATT CCG GTT ATG ATG ATG CCT GGG ACC AGG RMC GGY TTC      146
Pro Val Thr Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe
```


	-85	-80	-75	
GAA GRA AGA AWT TTC CGT GTG GAT GTA GTA CAC ATG GAT GAA AAC TCA				194
Glu Xaa Arg Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser				
	-70	-65	-60	
CTG GAG TTT GAC ATG GTG GGA ATT GAC GCA GCC ATT GCC AAT GCT TTT				242
Leu Glu Phe Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe				
	-55	-50	-45	
CGA CGA ATT CTG CTA GCT GAG GTG CCA ACT ATG GCT GTG GAG AAG GTC				290
Arg Arg Ile Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val				
	-40	-35	-30	
CTG GTG TAC AAT AAT ACA TCC ATT GTT CAG GAT GAG ATT CTT GCT CAC				338
Leu Val Tyr Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His				
	-25	-20	-15	-10
CGT CTG GGG CTC ATT CCC ATT CAT GCT GAT CCC CGT CTT TTT GAG TAT				386
Arg Leu Gly Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr				
	-5	1	5	
CGG AAC CAA GGA GAT GAA GAA GGC ACA GAG ATA GAT ACT CTA CAG TTT				434
Arg Asn Gln Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe				
	10	15	20	
CGT CTC CAG GTC AGA TGC ACT CGG				458
Arg Leu Gln Val Arg Cys Thr Arg				
	25	30		

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..172
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 234..316

id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 189..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 172..239
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..49
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..206
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 236..318
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 207..241
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 44..209
id AA181144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 235..317
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..48
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 225..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 209..240
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 185..334
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 169..318
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 46..169
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..50
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..219
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..205
id W04828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 252..334
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 236..318
id W04828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 341..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 323..362
id W04828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 221..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 206..241
id W04828
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..242
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq FEARIALPLLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATACTGCGAG T ATG GCG GCG TCA AAG GTG AAA CAG GAC ATG CCT CCG CCG	50
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro	
-75 -70 -65	
GGG GGC TAT GGG CCC ATC GAC TAC AAA CGG AAC TTR CCG CGT CGA GGA	98
Gly Gly Tyr Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly	
-60 -55 -50	
CTG TCG GGC TAC AGC ATG CTG GCC ATA GGG ATT GGA ACC CTG ATC TAC	146
Leu Ser Gly Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr	
-45 -40 -35	
GGG CAC TGG AGC ATA ATG AAG TGG AAC CGT GAG CGC AGG CGC CTA CAA	194
Gly His Trp Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln	
-30 -25 -20	
ATC GAG GAC TTC GAG GCT CGC ATC GCG CTG TTG CCA CTG TTA CAG GCA	242
Ile Glu Asp Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala	
-15 -10 -5	
GAA ACC GAC CGG ARG ACC TTG CAG ATG CTT CGG GAG AAC CTG GAG GAG	290
Glu Thr Asp Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu	
1 5 10 15	
GAG GCC ATC ATC ATG MAG GAC GTS CYC GAC TGG AAS GTG GGG RAA KVV	338
Glu Ala Ile Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa	

20

25

30

GHT GTT CCA CAC AAC CCG CTG GGT GCÇ CCC CTT GAT CGG GGA GCT
Xaa Val Pro His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
35 40 45

383

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 54..267
id AA027968
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 94..278
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..99
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 21..265
id HSC0SD021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..299

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..259
id T31694
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 116..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 61..219
id R38457
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..53
id R38457
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 219..253
id R38457
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 164..289
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq VLFFTGWWIIIDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
AAATGCGCGAC TGAGCCGGGT GGATGGTACT GCTGCATCCG GGTGTCTGGA GGCTGTGGCC 60
GTTTTGTTTT CTTGGCTAAA ATCGGGGGAG TGAGGCGGGC CGGCGCGGCG CGACACCGGG 120
CTCGGAACC ACTGCACGAC GGGGCTGGAC TGACCTGAAA AAA ATG TCT GGA TTT 175
                               Met Ser Gly Phe
                               -40
CTA GAG GGC TTG AGA TGC TCA GAA TGC ATT GAC TGG GGG GAA AAG CGC 223
Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp Gly Glu Lys Arg
-35 -30 -25
AAT ACT ATT GCT TCC ATT GCT GCT GGT GTA CTA TTT TTT ACA GGC TGG 271
Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe Phe Thr Gly Trp
-20 -15 -10
TGG ATT ATC ATA GAT GCA GCT GTT ATT TAT CCC ACC CGG 310
Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr Arg
```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 73..358
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 42..71
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 145..290
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 47..145
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 319..374
id AA159550

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 10..45
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 225..356
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LVFLTFLSIPSFV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```

AAGGTGCTCG TCATGCGCAA TGTGGCGCTG CGGCGGGCGG CAGGGCCTGT GTGTGCTGAG   60
GCGGCTGAGC GCGGACATG CACACCACAG AGCGTGGCGA TGGAACASTA ACCGGGCTTG   120
TGAGAGGGCT CTGCAGTATA AACTAGGAGA CAAGATCCAT GGATTCACCG TAAACCAGGT   180
GACATCTGTT CCCGAGCTGT TCCTGACTGC AGTGAAGCTC ACCC ATG ATG ACA CAG   236
                               Met Met Thr Gln

GAG CCA GGT ATT TAC ACC TGG CCA GAG AAA ACA CGA ATA ATC TGT TCA   284
Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg Ile Ile Cys Ser
-40                               -35                               -30                               -25

GCG TGC AGT TCC GTA CCA CTC CCA TGG ACA GTA CTG GTG TTC CTC ACA   332
Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu Val Phe Leu Thr
                               -20                               -15                               -10

TTC TTG AGC ATA CCG TCC TTT GTG GGT CTC AGA AAT ATC CGT GCA GAG   380
Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn Ile Arg Ala Glu
                               -5                               1                               5

ACC TTT CTT CAA AAT GTT   398
Thr Phe Leu Gln Asn Val
10

```

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(53..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 444..585
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(227..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 311..408
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 230..308
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 188..226
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 75..153
id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(275..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 156..205
id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 33..71

id R06283
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 328..384
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 286..342
id AA152388
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 131..183
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 89..141
id AA152388
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 283..324
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 242..283
id AA152388
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 42..85
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..44
id AA152388
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 351..406
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 312..367
id AA159107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 408..445
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 371..408
id AA159107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..225
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 166..198
id AA159107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(171..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 313..466
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(328..406)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 232..310
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(408..446)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 190..228
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 39..80
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq FLTALLWRGRIPG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGCGGAGACG CAGAGTCTTG AGCAGCGCGN CAGGCACC ATG TTC CTG ACT GCG CTC	56
Met Phe Leu Thr Ala Leu	
-10	
CTC TGG CGC GGC CGC ATT CCC GGC CGT CAG TGG ATC GGG AAG CAC CGG	104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg	
-5 1 5	
CGG CCG CGG TTC GTG TCG TTG CGC GCC AAG CAG AAC ATG ATC CGC CGC	152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg	
10 15 20	
CTG GAG ATC GAG GCG GAG AAC CAT TAC TGG CTG AGC ATG CCC TAC ATG	200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met	
25 30 35 40	
ACC CGG GAG CAG GAG CGC GGC CAC GCC SSG TTG CGC AGG AGG GAG GCC	248
Thr Arg Glu Gln Glu Arg Gly His Ala Xaa Leu Arg Arg Arg Glu Ala	
45 50 55	

```

TTC GAG GCS ATA AAG GCG GCC GCC ACT TCC AAG TTC CCC CCG CAT AGA      296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg
      60                      65                      70

TTC ATT GCG GAC CAG CTC GAC CAT CTC AVK VGT CAC CAA GAA ATG GTC      344
Phe Ile Ala Asp Gln Leu Asp His Leu Xaa Xaa His Gln Glu Met Val
      75                      80                      85

CTA ATC CTG AGT CGT CAC CCT TGG ATT TTA TGG ATC ACG GAG CTG ACC      392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr
      90                      95                      100

ATC TTT ACC TGG TCT GGA CTG AAA AAC TGT AGC TTG TGT GAA AAT GAG      440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu
      105                      110                      115                      120

CTT TGG ACC AGT CTT TAT                                          458
Leu Trp Thr Ser Leu Tyr
      125

```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..381
id W56872
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..291
id W31727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..354
id W16469
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..400
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..356
id N31028
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..354
id W16470
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..389
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```
AACTTGCTCT GAGACAGGTG CGGCAAGTCT ACTGCGGGCT GGTCCGGGCT CCTCAGGTTC      60
AGACCCGACC GTTATCCAGT CGGTTCGTGG AGAGGAGAGG TGSACTTTAC AGGTCCCCG      119
ATG AAC CAA GAG AAC CCT CCA CCA TAT CCA GGC CCT GGT CCA ACG GCC      167
Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
-90                -85                -80                -75
CCA TAC CCA CCT TAT CCA CCA CAA CCA ATG GGT CCA GGA CHT ATG GGG      215
Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly
-70                -65                -60
GGA CCC TAC CCA CCT CCT CAA GGG TAC CCC TAC CAA GGA TAC CCA CAG      263
Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln
-55                -50                -45
TAC GGC TGG CAG GGT GGA CCT CAG GAG CCT CCT AAA ACC ACA GTG TAT      311
Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
-40                -35                -30
GTG GTA GAA GAC CAA AGA AGA GAT GAG CTA GGA CCA TCC ACC TGC CTC      359
Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
-25                -20                -15
ACA GCC TGC TGG ACG GCT CTC TGT TGC TGC TGT CTC TGG      398
Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp
-10                -5                1
```

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..332
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..59
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 329..368
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..273
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 274..321
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..47
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 318..357
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..264
id W01758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 261..300
id W01758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 50..249
id W57829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..49
id W57829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..214
id HUM417E03B

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

AAGTTCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC AGG TCT      49
  Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser
                -50                      -45

CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA CAT TCG GTG      97
Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val
-40                -35                      -30

CTT TTA CCT ACC TAC AAC GAG CGC GAR GAA CTG CCG CTC ATC GTG TGG     145
Leu Leu Pro Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp
-25                -20                      -15                      -10

CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA ATT ATA     193
Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile
                -5                      1                      5

ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT GAA CAG     241
Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln
                10                      15                      20

TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA CGA GAG     289
Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu
                25                      30                      35

AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CAT GGA ATG RAA ACA TGC     337
Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys
40                45                      50                      55

CAC AGG RAA CTA CAT CAT TAT TAT GGA TGC                             367
His Arg Xaa Leu His His Tyr Tyr Gly Cys
                60                      65

```

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..408
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 61..399
id AA114853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..68
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..60
id AA114853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..391
id W23545
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 42..381
id AA069652
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..68
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..41
id AA069652
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 8..333
id AA084987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..347
id AA101916
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 303..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CPTCLCAPSXXWG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```
ATCCGGTGCA CGCGAGTSTT CTGAAACGTC AGCTGCGCTC CCCTAGGAGT GCTGAGCCCC 60
CGGAACCGCA GCCATGACTG AGGCTGATGT GAATCCAAAG GYCTATCCCC TTGCCGATGC 120
CCACCTCACC AAGAAGCTAC TGGACCTCGT TCAGCAGTCA TGTAActATA AGCAGCTTCG 180
GAAAGGWGCC AATGAGGCCA CCAAAACCCT CAACAGGGGC ATCTCTGAGT TCATCGTGAT 240
GGCTGCAGAC GCCGAGCCAC TGGAGATCAT TCTGCACCTG CCGCTGCTGT GTGAAGACAA 300
GA ATG TGC CCT ACG TGT TTG TGC GCT CCA AGC AVN SCC TGG GGA GAG 347
  Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu
      -10                      -5                      1

CCT GTG GGG TCT CCA GGC CTG TCA TCG CCT GTT CTG TCA CCA TCA AAG 395
Pro Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys
      5                      10                      15

AAG GCT CGC AGC 407
Lys Ala Arg Ser
      20
```

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 34..159
id N52621
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..38

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..31
id N52621
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 5..152
id AA157163
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 10..66
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq AVAASAASGQAEG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
ACTTCTAAG ATG GCT GCC GCT ACC GGT GCG GTG GCA GCC TCG GCC GCC TCG    51
  Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser
                    -15                               -10

GGT CAG GCG GAA GGT AAA AAG ATC ACC GAT CTG CGG GTC ATC GAT CTG    99
Gly Gln Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu
-5              1              5              10

AAG TCC GAG CTG AAG CGG CGG AAC TTA GAC ATC ACC GGA GTC AAG ACC    147
Lys Ser Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr
          15              20              25

GTG CTC ATC TCC CGA CTA AGG    168
Val Leu Ile Ser Arg Leu Arg
          30
```

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..343

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..306
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..103
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 340..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 304..397
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..388
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..401
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..356
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..389
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 82..339
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 50..139
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..90
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 387..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 338..384
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 126..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 75..382
 id H29689
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 23..73
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq SLLXRVSVTAVAA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

ATTCTCCTG CCCGTAGTAG CC ATG GCG GCC ATG AGT TTG TTG CKG CGG GTT	52
Met Ala Ala Met Ser Leu Leu Xaa Arg Val	
-15 -10	
TCG GTT ACT GCG GTG GCA GCT CTG TCT GGC CGG CCC CTT GGC ACY NGC	100
Ser Val Thr Ala Val Ala Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa	
-5 1 5	
CTC GGA TTT GGG GGC TTC CTC ACT CGT GGC TTT CCG AAG GCT GCT GCT	148
Leu Gly Phe Gly Gly Phe Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala	
10 15 20 25	
CCT GTT CGA CAC AGT GGA GAC CAT GGG AAA AGA CTA TTT GTC ATC AGA	196
Pro Val Arg His Ser Gly Asp His Gly Lys Arg Leu Phe Val Ile Arg	
30 35 40	

CCT TCT AGA TTC TAT GAC AGG CGT TTT TTG AAG TTA TTG AGA TTC TAC	244
Pro Ser Arg Phe Tyr Asp Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr	
45 50 55	
ATT GCA TTG ACT GGG ATT CCA GTA GCA WTT TTC ATA ACT CTG GTG AAT	292
Ile Ala Leu Thr Gly Ile Pro Val Ala Xaa Phe Ile Thr Leu Val Asn	
60 65 70	
GTA TTC ATT GGT CAA GCT GAA CTA GCA GAA ATT CCA GAA GGC TAT GTC	340
Val Phe Ile Gly Gln Ala Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val	
75 80 85	
CCA GAA CAC TGG GAA TAT TAT AAG CAT CCC ATA TCA AGA TGG ATT GCC	388
Pro Glu His Trp Glu Tyr Tyr Lys His Pro Ile Ser Arg Trp Ile Ala	
90 95 100 105	
CGT AAT TTC TAT GAT AGT CCT GMA AAG ATA TAT GAA AGA ACA ATG	433
Arg Asn Phe Tyr Asp Ser Pro Xaa Lys Ile Tyr Glu Arg Thr Met	
110 115 120	

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..452
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..409
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..54
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 107..404
id AA088577

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..100
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 29..96
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 6..41
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..36
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..189
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 7..156
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 156..279
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 46..207
id H85485
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LDLLRGLPRVSLA/NL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

GAGACCACGT GGCCTCCGAG CACCTCAGGG CGCCCTTGAA AGTTCTTGA TCTGCGGGTT 60

ATG GCC GGT CCC TTG CAG GGC GGT GGG GCC CGG GCC CTG GAC CTA CTC 108
Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu

-25	-20	-15	-10	
CGG GGC CTG CCG CGT GTG AGC CTG GCC AAC TTA AAG CCG AAT CCC GGC				156
Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly				
	-5	1	5	
TCC AAG AAA CCG GAG AGA AGA CCA AGA GGT CGG AGA AGA GGT AGA AAA				204
Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Gly Arg Lys				
	10	15	20	
TGT GGC AGA GGC CAT AAA GGA GAA AGG CAA AGA GGA ACC CGG CCC CGC				252
Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg				
	25	30	35	
TTG GGC TTT GAG GGA GGC CAG ACT CCA TTT TAC ATC CGA RTC CCA AAA				300
Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys				
	40	45	50	55
TAC GGG TTT AAC GAA GGA CAT AGT TTC AGA CGC CAG TAT AAG CCT TTG				348
Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu				
	60	65	70	
AGT CTC AAT AGA CTG CAG TAT CTT ATT GAT TTG GGT CGT GTT GAT CCT				396
Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro				
	75	80	85	
AGT CAA CCT ATT GAC TTA ACC CAG CTT GTC AAT GGG AGA GGT GTG ACC				444
Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr				
	90	95	100	
ATC GCG CCG				453
Ile Ala Pro				
	105			

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..103
id T11164
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 133..223
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 102..192
 id T11164
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq GILILWIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

AAAGGAAGCG GCTAACT ATG GCG ACC GCC ACG GAG CAG TGG GTT CTG GTG      50
Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val
-40 -35

GAG ATG GTA CAG GCG CTT TAC GAG GCT CCT GCT TAC CAT CTT ATT TTG      98
Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu
-30 -25 -20 -15

GAA GGG ATT CTG ATC CTC TGG ATA ATC AGA CTT CTT TTC TCT AAG ACT      146
Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr
-10 -5 1

TAC AAA TTA CAA GAA CGA TCT GAT CTT ACA GTC AAG GAA AAA GAA GAA      194
Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu
5 10 15

CTG ATT GAA GAG TGG CAA CCA GAA CCT CTT GTT CCT CCT GTC CCA AAA      242
Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys
20 25 30

GAC CAT CCT GCT CTC AAC TAC AAC ATC GTT TCA GGC CCT CCA AGC CAC      290
Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His
35 40 45 50

AAA ACT GTG GTG AAT GGA AAA GAA TGT ATA AAC TTC GCC TCA TTT AAT      338
Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn
55 60 65

TTT CTT GGA TTG TTG GAT AAC CCT AGG GTT AAG GCA GCA GCT TTA GCA      386
Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala
70 75 80

TCT CTA AAG AAG TAT GGC GTG GGG ACT TGT GGA CCC TGT      425
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys
85 90 95

```

(2) INFORMATION FOR SEQ ID NO: 256:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs
 (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 124..305
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..123
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..361
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..144
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 145..274
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 276..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 275..308
id H23328

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 146..308
id H06320
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 69..145
id H06320
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..40
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..36
id H06320
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 222..258
id T62768
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 162..398
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq QGVLFICFTCARS/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```
AAAACTGAG GCCTGGGAGC AGGAACCTGT AGGCAGCGCT TGAGGGTAGC GGGATAGCAG 60
CTGCAACGCG CGTGGGAGGC GGGGGCTCTG GGCGGAACAA AAATCACAGG ATGTCAGAGG 120
ATGTTTCCCG GGAAGAACTG GGATAAAGGG GTCCCAGCAC C ATG GAG GAC CCG AAC 176
                                         Met Glu Asp Pro Asn
                                         -75

CCT GAA GAG AAC ATG ADG CAG CAG GAT TCA CCC AAG GAG AGA AGT CCC 224
Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
-70 -65 -60

CAG AGC CCA GGA GGC AAC ATC TGC CAC CTG GGG GCC CCG AAG TGC ACC 272
```

Gln	Ser	Pro	Gly	Gly	Asn	Ile	Cys	His	Leu	Gly	Ala	Pro	Lys	Cys	Thr		
			-55					-50					-45				
CGC	TGC	CTC	ATC	ACC	TTC	GCA	GAT	TCC	AAG	TTS	SAG	GAG	CGT	CAC	ATG	320	
Arg	Cys	Leu	Ile	Thr	Phe	Ala	Asp	Ser	Lys	Xaa	Xaa	Glu	Arg	His	Met		
		-40					-35					-30					
AAG	CGG	GAG	CAC	CCA	GCG	GAC	TTC	GTG	GCC	CAG	AAG	CTG	CAG	GGG	GTC	368	
Lys	Arg	Glu	His	Pro	Ala	Asp	Phe	Val	Ala	Gln	Lys	Leu	Gln	Gly	Val		
	-25					-20				-15							
CTC	TTC	ATC	TGC	TTC	ACC	TGC	GCC	CGC	TCC	TTC	CCC	TCT				407	
Leu	Phe	Ile	Cys	Phe	Thr	Cys	Ala	Arg	Ser	Phe	Pro	Ser					
-10					-5					1							

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(166..452)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..302
id AA062591
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..45
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 43..89
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..45
id AA158431
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 444..490
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 43..89
id AA158431
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..160
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```
AAGGATCCTC TACCGGCTTT TCGAGTCAGT GCTGCCGCCG CTGCCCGCGG CTTTGCAGAG    60
CAGG ATG AAT GTG ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG    109
      Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu
      -30                -25                -20
CAC TCC AAC GTG CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT    157
      His Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn
      -15                -10                -5
AAC AAC CCT GAG TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG    205
      Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val
      1                5                10                15
TAT CAT GCA GAT TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG    253
      Tyr His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val
      20                25                30
AGT AAG TAT ACC ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT AAA ACT    301
      Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr
      35                40                45
TCA AAA GTG AGA CCT TCA ACT GGA AAT TCT GCA TCT ACT CCA CAA AGT    349
      Ser Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser
      50                55                60
CAG TGT CTT CCA TCT GAA ATT GAA GTG AAA TAC AAA ATG GCT GAA TGT    397
      Gln Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys
      65                70                75
TAT ACA ATG CTA AAA CAA GAT AAA GAT GCC ATT GCT ATA CTT GAT GGG    445
      Tyr Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly
      80                85                90                95
KST CCC TTC AAG ACA AAG AAC TCC CAR AAT AAA CAT GAT GCT GGC    490
      Xaa Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly
```

100

105

110

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..312
id HSC26F061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 20..260
id W30546
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 66..252
id H34739
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGGGTGCTGC CWKCCGGGTG CTGWTGCGAG TCGGTGGCAG CGAGGACATT TTCTGACTCC 60

CTGGCCCTG ACACGGCTGC ACTTCCATC CCGTCGCGGG GCCGGCCGCT ACTCCGGCCC 120

CAGG ATG CAG AAT GTG ATT AAT ACT GTG AAG GGA AAG GCA CTG GAA GTG 169

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val

	-55	-50	-45	
GCT GAG TAC CTG ACC CCG GTC CTC AAG GAA TCA AAG TTT AAG GAA ACA				217
Ala Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr				
	-40	-35	-30	
GGT GTA ATT ACC CCA GAA GAG TTT GTG GCA GCT GGA GAT CAC CTA GTC				265
Gly Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val				
	-25	-20	-15	
CAC CAC TGT CCA ACA TGG CAA TGG GCT ACA GGG GAA GAA TTG AAA GTG				313
His His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val				
	-10	-5	1	5
AAG GCA TAC CTA CCA ACA GGC AAA TGG				340
Lys Ala Tyr Leu Pro Thr Gly Lys Trp				
	10			

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 89..262
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..428
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 334..402
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 260..321
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 428..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 401..438
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 62..285
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..43
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 401..444
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 312..345
id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 283..313
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 102..264
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 336..441
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 262..323
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 28..79
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 78..254
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 252..313
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..69
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..373
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 209..472
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```
AGATCCCGCC TGGGGCCGGC TGAGTGGCAC TTAAGCGGGC CATGCCATGC AACCTTGGGC   60
GCTGCCAACC GTGGGCGAGC TCTGGGTGTG CGGGCGGCCT GCGCGGGCGC TCCGCTGTCT  120
CAGCGTGTTA TGATCCGTC CCGTACCAAC CTGGCTACTG GAATCCCCAG TAGTAAAGTG  180
AAATATTCAA GGCTCTCCAG CACAGACG ATG GCT ACA TTG ACC TTC AGT TTA      232
                               Met Ala Thr Leu Thr Phe Ser Leu
                               -85

AGA AAA CCC CTC CAA AGA TCC CTT ATA AGG CCA TCG CAC TTG CCA CTG      280
Arg Lys Pro Leu Gln Arg Ser Leu Ile Arg Pro Ser His Leu Pro Leu
-80                               -75                               -70                               -65

TGC TGT TTT GAT TGG CGC CTT TCT CAT TAT TAT AGG CTC CCT CCT GCT      328
Cys Cys Phe Asp Trp Arg Leu Ser His Tyr Tyr Arg Leu Pro Pro Ala
-60                               -55                               -50

GTC AGG CTA CAT CAG CAA AGG GGG GGC AGA CCG GGC CGT TCC AGT GCT      376
Val Arg Leu His Gln Gln Arg Gly Gly Arg Pro Gly Arg Ser Ser Ala
```

-45

-40

-35

GAT CAT TGG CAT TCT GGT GTT CCT ACC CGG ATT TTA CCA CCT GCG CAT 424
Asp His Trp His Ser Gly Val Pro Thr Arg Ile Leu Pro Pro Ala His
-30 -25 -20

CGC TTA CTA TGC ATC CAA AGG CTA CCG TGG TTA CTC CTA TGC AGG GGG 472
Arg Leu Leu Cys Ile Gln Arg Leu Pro Trp Leu Leu Leu Cys Arg Gly
-15 -10 -5

ATC ACT AGT 481
Ile Thr Ser
1

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 67..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 51..202
id N55991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..59
id N55991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..143
id R57473
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..339
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 143..250
id R57473
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..243
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 195..298
id H79944
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 243..279
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 299..335
id H79944
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 97..194
id H70394
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 235..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 193..293
id H70394
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 80..265
id W31972
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 123..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq PS LAAGLLFGSXA/GL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

TCCGCGGGGCC TTCGGCAGAT GCAGGCCTGG GGTAGTCTCC TTTCTGGACT GAGAAGAGAA 120
GA ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC 167
  Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
      -45 -40 -35

TTT GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA 215
Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
      -30 -25 -20

AAA ACA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTC GGC AGT 263
Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
      -15 -10 -5

VWA GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCA AGR AAC GTT 311
Xaa Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
      1 5 10

TGG GGT TTC CTA GCC GCT ACA TCT GTT 338
Trp Gly Phe Leu Ala Ala Thr Ser Val
  15 20

```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..238
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..89
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 162..298
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 116..252
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..56
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 61..98
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 59..159
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 194..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 159..206
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 14..56
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 32..228
id H35655
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 108..304
id AA038389
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 108..161
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
AGGGGGTTGC GTCGCTCTCT GTTAAAGGCG TGCAGGTGTT GGCCGCGGCC TCTGAGCTGG      60
GATGAGCCGT GCTCCCGGTG GAAGCAAGGG GAGCCCCAGC SGGAGCC ATG GCC AGT      116
                                         Met Ala Ser
ACA GTG GTA GCA GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC      164
Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly
-15          -10          -5          1
CGT TAC GTT TTG CAA GCC ATG AAG CAT ATG GAG CBT CAA GTA AAA CAA      212
Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln Val Lys Gln
          5          10          15
GTT TTT CAA AGC CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA      260
Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg
          20          25          30
GGT BGG TTT GAA CCC ARA ATG RCA AAA CGG GAA GCA GCG GGG      302
Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala Gly
          35          40          45
```

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 96..277
id T32007

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..98
id T32007
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R59039
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 19..78
id R59039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 70..254
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..72
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 136..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

AAAGTTCTCC TTCCACCTTC CCCCACCCTT CTCTGCCAAC CGCTGTTTCA GCCCCTAGCT    60
GGATTCACAGC CATTGCTGCA GCTGCTCCAC AGCCCTTTTC AGGACCCAAA CAACCGCAGC    120
CGCTGTTCCC CAGGR ATG GTG ATC CGT GTA TAT ATT GCA TCT TCC TCT GGC    171
      Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
      -80                               -75

TCT ACA GCG ATT AAG AAG AAA CAA CAA GAT GTG CTT GGT TTC CTA GAA    219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-70                               -65                               -60

GCC AAC AAA ATA GGA TTT GAA GAA AAA GAT ATT GCA GCC AAT GAA GAG    267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-55                               -50                               -45                               -40

AAT CGG AAG TGG ATG AGA GAA AAT GTA CCT GAA AAT AGT CGA CCA GCG    315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
      -35                               -30                               -25

GTT CAG GGG CCA CAT GCT TTT CGG TAT AAA GCA TTC TCC TTC TCT AGG    363
Val Gln Gly Pro His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg
      -20                               -15                               -10

TTG CTA TCA CAG TGC AGA CCT GAC TGC CTG AAT ATG CTC AGG AGA TTT    411
Leu Leu Ser Gln Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe
      -5                               1                               5

AGT CAA TAT TGT CTG TAT TTG GTT ATG GAA AAG GCT CTC CTT TTT TTT    459

```

Ser Gln Tyr Cys Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe
10 15 20 25

TTT TTT
Phe Phe

465

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 117..274
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..116
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..355
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 270..302
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..330

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 113..311
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 36..112
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..41
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..330
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 94..292
id R25047
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 17..93
id R25047
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..352
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 38..331
id R23993
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 163..294
id W23811
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..194
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 131..193
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 305..354
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 308..357
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 350..390
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 354..394
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 243..368
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq ITSSLFLGRGSA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AAGAAGCCGG TGGCCGCGCA GGAGGACGGA GCCCTAACCG CAACCCGCGC CGCGCCGCGC   60
CGATTTGATT TGTATCCACT GTCACCAGCA CTGCTCACTT AGGACTTTCT GGATCCAGAC   120
CCAGGCAGCG CACACTGGAC TCTTGAGGAA GAAGGAGACT CTAATTTTGG ATTCCTTGGT   180
GGAGGAAAAT AAAAACTCT GGTCTTGCCG CCAACGATGC AAGTGTGACT GCTGGCGTCT   240
TC ATG AGC TCC AGA GGT CAC AGC ACG CTA CCA AGG ACT CTC ATG GCC   287
  Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala
    -40                      -35                      -30

CCT CGG ATG ATT TCC GAG GGA GAC ATA GGA GGC ATT GCT CAA ATC ACC   335
Pro Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr
  -25                      -20                      -15

TCC TCT CTA TTC CTG GGC AGA GGC AGT GTG GCC TCC AAT CGG CAC CTC   333
Ser Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu
  -10                      -5                      1                      5

CTC CAG GCT CGT GGC ATC   401
Leu Gln Ala Arg Gly Ile
      10

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..183
id AA022583
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(69..228)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 281..440
id AA022584
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 66..119
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
AGGAAGTTCC GGGCCGAGTT CCTCGTGCCA ACGTGTCTTG TAAGGTGCGG CTAGAAACTG      60
GGGAC ATG GCA GCG CCT GGC CCA GCG CTC TGC CTC TTC GAC GTG GAT GGG      110
      Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly
                -15                -10                -5

ACC CTC ACC GCC CCG CGG CAG AAA ATT ACC AAA GAA ATG GAT GAC TTC      158
Thr Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe
                1                5                10

CTA CAA AAA TTG AGG CAG AAG ATC AAA ATC GGA GTG GTA GGC GGA TCG      206
Leu Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser
      15                20                25

GAC TTT GAG AAA GTG CAG GAA CGG      230
Asp Phe Glu Lys Val Gln Glu Arg
      30                35
```

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 159..278
id H97759
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 107..160
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 166..250
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 114..167
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 143..201
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..51
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 200..229
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 170..247
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 121..171
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 240..285
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..90
id N56221
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 126..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
ACTGGAAGAA CTCGTCATGC TCTTTGTAGC GTGGTGCTTC TGTTGCTCAC AGGACAACCTT   60
GCCTTTGATG ATTTTCAAGA GAGTTGTGCT ATGATGTGGC AAAGTATGCA GGAAGCAGGC   120
GGTCA ATG CCT CTG GGA GCA AGG ATC CTT TTC CAC GGT GTG TTC TAT GCC   170
      Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
                -15                      -10                      -5
GGG GGC TTT GCC ATT GTG TAT TAC CTC ATT CAA AAG TTT CAT TCC AGG   218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
                1                      5                      10
ACA CTG   224
Thr Leu
```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
 region 1..215
 id HUM429E03B
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 235..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
 region 211..303
 id HUM429E03B
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
 region 107..310
 id T80259
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 15..114
id T80259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..245
id T31768
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 271..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 234..290
id T31768
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 47..272
id N32697
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..43
id N32697
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..263
id N44613
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 156..194
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GCCTAGGTGT TGTCGTCCCT GCTAGTACTC CGGGCTGTGG GGGTCGGTGC GGATATTCAG      60
TCATGAAATC AGGGTAGGGA CTTCTCCCGC AGCGACGCGG CTGGCAAGAC TGTTTGTGTT      120
GCGGGGGCCG GACTTCAAGG TGATTTTACA ACGAG ATG CTG CTC TCC ATA GGG          173
                               Met Leu Leu Ser Ile Gly
                               -10

ATG CTC ATG CTG TCA GCC ACA CAA GTC TAC ACC ATC TTG ACT GTC CAG          221
Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln
      -5                      1                      5

CTC TTT GCA TTC TTA AAC CTA CTG CCT GTA GAA GYA GAC ATT TTA GCA          269
Leu Phe Ala Phe Leu Asn Leu Leu Pro Val Glu Xaa Asp Ile Leu Ala
      10                      15                      20                      25

TAT AAC TTT GAA AAT GCA TCT CAG ACA TTT GAT GAC CTC CCT GCA AGA          317
Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Arg
                      30                      35                      40

TTT GGT TAT                                                                326
Phe Gly Tyr

```

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..368
id AA150637
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 30..294
id H02768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..372
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 148..339
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..147
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(267..394)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 231..358
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(184..277)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 349..442
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(109..164)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 464..519
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 72..250
id N30922
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..180
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..64
id N30922
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

AATCGCGGAG TCGGTGCTTT AGTACGCCGC TGGCACCTTT ACTCTCGCCG GCCGCGCGAA   60
CCCGTTTGAG CTCGGTATCC TAGTGACAC GCCTTGCAAG CGACGGCGCC ATG AGT   116
                                     Met Ser
                                     -25

CTG ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC   164
Leu Thr Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
      -20                      -15                      -10

ATT GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT   212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
      -5                      1                      5

TAT GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG   260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
    10                      15                      20                      25

AAA GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTS RNA   308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Xaa Xaa
      30                      35                      40

GAT AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC   356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
      45                      50                      55

TGT GAT GGG GCT CAC ACA ARM VAT AAC GAA GAG ACT GGG CTG   398
Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
    60                      65                      70

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..150
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 31..126
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 151..212
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 126..187
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..35
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 211..242
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 185..216
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..263
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 202..410
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 172..206
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 159..230
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 174..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 279..340
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 129..163
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 189..299
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 298..338
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 159..193
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 201..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 337..371
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..252
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq YTAHSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AATTACGCAG AGAGAAAGTT ACGAGAAACT CGTTTTCATC TTCTTGTTT CATCYTAAAT   60
ACCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA GAA AAT TCT CAC AAT AAG   111
      Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys
      -60                               -55                               -50

GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA GTT GAA CGA AGC CAG GTT   159
Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val
      -45                               -40                               -35

CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG TGG CAA GAC TAT AAG CCT   207
Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro
      -30                               -25                               -20

GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT GGA CCC AGG TGG GCA GAT   255
Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp
      -15                               -10                               -5                               1

CCT CAG ATC AGT GAV AGT VAT TTT TCT CCC AAG TTT AAC GAA AAG GAT   303
Pro Gln Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp
      5                               10                               15

GGG CAT GTT GAG AGA NAG AGC AAG AAT GGC CTG TAT GAG ATT GAN AAT   351
Gly His Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn
      20                               25                               30

GGA AGA CCG AGA AAT CCT GCA GAC GGA CTG GAC TGG TGG GCC   393
Gly Arg Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
      35                               40                               45

```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 137..335
id HSC1QH021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 126..263
id HUML12288
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..87
id HUML12288
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 178..443
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..266
id R60742
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..303
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 133..232
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 35..129
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..49
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..32
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 136..280
id C04685
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..147

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 10..132
id C04685
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 349..438
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
AAAACCTTAG CAAGATGGCG GCTCCCTGGG CGTCCCTGCG CCTGGTCGCC CCCATGTGGA    60
ATGGGCGTAT CAGGGGCATC CATCGCCTGG GTGCGGCAGT GGCCCCAGAG GGCAATCAGA    120
AGAAGAAAAG GACAATAMTC CARKTYCCTG GMCCVAASTA TTTCTACGAT GTGGAGGCTC    180
TGAGGGATTA CTTGCTCCAA AGGGAGATGT ACAAGGTGCA TGAGAAAAAT CGATCTTACA    240
CCTGGCTGGA GAAGCAACAT GGTCCATACG GCGCAGGTGC CTTTTTCATC CTGAAGCAGG    300
GAGGCGCAGT CAAGTTTCGA GACAAGGAGT GGATCAGGCC AGATAAGT ATG GCC ATT    357
                               Met Ala Ile
                               -30

TCT CTC AGG AGT TCT GGA ATT TCT GTG AAG TGC CTG TCG AAG CTG TGG    405
Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser Lys Leu Trp
   -25                -20                -15

ATG CGG TGG ACT GTG ACA TCA ACT ACG AGG GCC TGG ATM RNN GCN GAA    453
Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile Xaa Ala Glu
   -10                -5                1                5

CCT CCG CAG CTG GAC ATC TCG    474
Pro Pro Gln Leu Asp Ile Ser
                10
```

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 82..210

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 49..177
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..83
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 15..51
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 17..97
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FVLGSARLGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```
AACATTAACC GGCAGG ATG TCG GAG GTG CGG CTG CCA CCG CTA CGC GCC CTG   52
      Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu
      -25                                -20

GAC GAC TTT GTT CTG GGG TCG GCG CGT CTT GGC GGC TCC GGA TCC ATG   100
Asp Asp Phe Val Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met
-15              -10              -5              1

CGA CCC GCT GCG ATG GTG YHA CCG CGT CAT CAA CAA CCT CCT CTA CTA   148
Arg Pro Ala Ala Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu
      5              10              15

CCA AAC CAA CTA CCT TCT CTG CTT CGG CAT CGG CCT CGC TCT CGC CGG   196
Pro Asn Gln Leu Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg
      20              25              30

GTA CGT ACG GCC ACG   211
Val Arg Thr Ala Thr
      35
```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 177..257
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 107..177
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 52..102
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 132..174
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id N44655
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 104..174
id N44655

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..170
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..226
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..40
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 63..169
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 169..249
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..39
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 206..250
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
AGGCGGCGAA GATGGCGGAG AACAGCGGTC GCGCCGGCAA GAGCAGCGGG AGCGNCGCGN 60
GGAAGGGGGC GGTGTCCGCA GAGCAGGTGA TTGCTGGCTT CAACCGCCTT CGGCAGGAAC 120
AGCGAGGCCT GGCATCCAAA GCAGCTGAGT TGGAGATGGA GTTGAATGAG CACAGCCTAG 180
TGAATCGATA CACTGAAGGA GGTAG ATG AAA CTC GTA AGT GCT ACC GCA TGG 232
                               Met Lys Leu Val Ser Ala Thr Ala Trp
                               -15                               -10
TTG GAG GAR TGC TGG TGG AGC GAA CTG TCA 262
Leu Glu Glu Cys Trp Trp Ser Glu Leu Ser
-5                               1
```

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 142..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 120..360
id HUML1108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 17..127
id HUML1108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 37..395
id AA156844
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..395
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 137..500
id HSU51712
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 237..395
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 112..270
id T70871
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 133..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 9..111
id T70871
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..185
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 105..213
id H48308
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 177..286
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 206..315
id H48308
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 284..317
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 314..347
id H48308
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 309..410
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.3
seq LYVPLLAVCCCLRS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

AAGCTTCCAA ACCCAGGGCT TGCCTTGCC TTGCCTCTT CCACCGCGCA GGGACCATGT   60
CGGCGGAGAC CGCGAGCGGC CCCACAGAGG ACCAGGTGGA AATCCTGGAG TACAACTTCA  120
ACAAGGTCGA CAAGCACCCG GATTCCACCA CGCTGTGCCT CATCGCGGCC GAGGCAGGCC  180
TTCCGAGGA GGAGACCCAG AAATGGTTTA AGCAGCGCCT GGCAAAGTGG CGGCGCTCAG  240
AAGGCCTGCC CTCAGAGTGC AGATCCGTCA CAGACTAAGG AGATGGCAGG CATTGACAGC  300
TTCCTCC ATG AAG GCC ATC TCT GTT TCT CTC CTC CGC TTA ACC AAG CTG   350
      Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu
                -30                                -25

TTG TGG TTT TTC AGC ATA GTG TTG TAT GTT CCA TTG CTA GCT GTC TGC   398
Leu Trp Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys
-20                -15                                -10                                -5

TGT TTA CAC AGT GTT GTA TTT TTT                                     422
Cys Leu His Ser Val Val Phe Phe
                1

```

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..421
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 179..405
id AA010986
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..91
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 108..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 91..188
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 443..505
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 429..491
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 417..449
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 402..434
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..187
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..494
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 300..478
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 195..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 178..319
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..513
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..445
id W44481
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..193
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 184..289
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 340..396
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 301..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 291..342
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 405..448
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 397..440
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..222
id W40172
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..439
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 343..440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

ACTCCAACGC TGGGTGACAT TGAGCTCACC AGCGCCACCG TCCCGGCGCA AGTTCTGCGC	60
TGGTCGGCGG AGTAGCAAGT GGCC ATG GGG AGC CTC AGC GGT CTG CGC CTG	111
Met Gly Ser Leu Ser Gly Leu Arg Leu	-115 -110
GCA GCA GGA AGC TGT TTT AGG TTA TGT GAA AGA GAT GTT TCC TGN TCT	159
Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Xaa Ser	-105 -100 -95
CTA AGG CTT ACC AGA AGC TCT GAT TTA AAG AGA ATA AAT GGA TTT TGC	207
Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys	-90 -85 -80
ACA AAA CCA CAG GAA AGT CCC GGA GCT CCA TCC CGC ACT TAC AAC AGA	255
Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg	-75 -70 -65
GTG CCT TTA CAC AAA CCT ACG GAT TGG CAG AAA AAG ATC CTC ATA TGG	303
Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp	-60 -55 -50
TCA GGT CGC TTC AAA AAG GAA ANB NAA ATC CCA GAG ACT GTC TCG TTG	351
Ser Gly Arg Phe Lys Lys Glu Xaa Xaa Ile Pro Glu Thr Val Ser Leu	-45 -40 -35 -30
GAG ATG CTT GAN STT GCA AAG AAC AAG ATG CGA GTG AAG ATC AGC TAT	399
Glu Met Leu Xaa Xaa Ala Lys Asn Lys Met Arg Val Lys Ile Ser Tyr	-25 -20 -15
CTA ATG ATT GCC CTG ACG GTG GTA GGA TGC ATC TTC ATG GTT ATT GAG	447
Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met Val Ile Glu	-10 -5 1
GGC AAG AAG GCT GCC CAA AGA CAC GAG ACT TTA ACA AGC TTG MAC TTA	495
Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser Leu Xaa Leu	5 10 15
GAA AAG AAA GCT CGT CTG	513

Glu Lys Lys Ala Arg Leu
20 25

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 190..399
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..141
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 139..198
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 139..341
id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..147

id N42162
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 198..354
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 144..300
id N24414
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 10..95
id N24414
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 93..152
id N24414
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 198..414
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 122..339
id W76137
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 75..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..73
id W76137
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 71..130
id W76137
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 198..360
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 121..283
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..72
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 346..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 270..326
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 70..129
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..358
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LASSFLFTMGGLG/FI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

ACTGTTTNGG	GGAGGCGCGT	GGGGCTTGAG	GCCGAGAACG	GCCCTTGCTG	CCACCAAC	58
ATG GAG ACT TTG TAC CGT GTC CCG TTC TTA GTG CTC GAA TGT CCC AAC	106					
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn						
-100 -95 -90 -85						
CTG AAG CTG AAG AAG CCG CCC TGG TTG CAC ATG CCG TCC GCC ATG ACT	154					
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr						
-80 -75 -70						
GTG TAT GCT CTG GTG GTG GTG TCT TAC TTC CTC ATC ACC GGA GGA ATA	202					
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile						
-65 -60 -55						
ATT TAT GAT GTT ATT GTT GAA CCT CCA AGT GTC GGT TCT ATG ACT GAT	250					
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp						
-50 -45 -40						
GAA CAT GGG CAT CAG AGG CCA GTA GCT TTC TTG GCC TAC AGA GTA AAT	298					

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 -35 -30 -25

GGA CAA TAT ATT ATG GAA GGA CTT GCA TCC AGC TTC CTA TTT ACA ATG 346
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 -20 -15 -10 -5

GGA GGT TTA GGT TTC ATA ATC CTG GAC GGA TCG RNT GCA CCA AAT ATC 394
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile
 1 5 10

CCA AAA CTC AAT AGA TTC 412
 Pro Lys Leu Asn Arg Phe
 15

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
 region 80..132
 id C05215
 est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
 seq MLVLRSGLTALA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CACTCGGGAA GACTTCAGAG AAGTCTCACA AAGGACTCGG CTGGCTGCTT TTCTCAGTGC 60

CGAAGCCGCG CC ATG CTC GTT CTC AGA AGC GGC CTG ACC AAG GCG CTT GCC 111
 Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala
 -10 -5

TCA CGG ACG CTC GCG CVT CAG AKA AWT TTT GCT CAT CGA GCT GAA GTT 159
 Ser Arg Thr Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val
 1 5 10 15

CGG AAA GCG TTA GCC AAC TGT AAG GAA TGG CAA GAA CAA TCT ATC ATT 207

Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile
20 25 30

CCA AAT TTG GCT CGC ATT GAT AAA CAA GAG ACC AGG 243
Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 77..206
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..77
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..194
id HUM427G10B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..65
id HUM427G10B
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 112..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 52..181
id R52722
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..52
id R52722
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 79..209
id W41484
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 30..137
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq NIESLAWTGGTG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GAGTTTCCTG	CGAGCTCGGC	TTCCTCAAC	ATG	GCT	GCG	CCC	TTG	TCA	GTG	GAG	53
	Met	Ala	Ala	Pro	Leu	Ser	Val	Glu			
	-35								-30		
GTG	GAG	TTC	GGA	GGT	GGT	GCG	GAS	TCC	TGT	TTG	101
Val	Glu	Phe	Gly	Gly	Gly	Ala	Xaa	Ser	Cys	Leu	
	-25					-20				-15	
ATC	GAG	TCA	CTT	GCC	TGG	ACA	GGA	GGA	ACC	CTG	149
Ile	Glu	Ser	Leu	Ala	Trp	Thr	Gly	Gly	Thr	Leu	
	-10				-5				1		
GCT	CAT	CTG	GAT	CAA	GAA	GAA	TTT	GCT	AAA	AGA	197
Ala	His	Leu	Asp	Gln	Glu	Glu	Phe	Ala	Lys	Arg	
5				10				15		20	
CAT	CCA	GGG	AGA	CAG	CGT	GCG	GCC	AGG	AAT	TCT	245
His	Pro	Gly	Arg	Gln	Arg	Ala	Ala	Arg	Asn	Ser	
		25				30				35	

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..382
id AA127626
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 44..329
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 330..384
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..60
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..39
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 68..424
id N32838
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(56..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 67..414

id AA121528
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 164..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 130..344
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 36..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..130
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..392
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACTTAGTCGT GTGTACATCA TTGGGAATGG AGGGAAATAA ATGACTGGAT GGTGCTGCT 60
TTTTAAGTTT CAAATTGACA TTCCAGACAA GCGGTGCCTG AGCCTGTGCC TGTCTTCAGA 120
TCTTCACAGC ACASTTCCTG GGAAGGTGGA GCCACCAGCC TCTCCTGAA TAACTGGGAG 180
ATGPAACAGG AAGCTCT ATG ACA CAC TTG ATC GAA TAT GAC AGA CAC CGA 230
      Met Thr His Leu Ile Glu Tyr Asp Arg His Arg
      -65                -60                -55
AAA TCA CGA CTC AGC CCC CTC CAG CAC CTC TAC CTG TTG CCC GCC GAT 278
Lys Ser Arg Leu Ser Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp
      -50                -45                -40
CAC AGC CGG AAT GCA GCT GAA AGA TTC CCT GGG GCC TGG TTC CAA CCG 326
His Ser Arg Asn Ala Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro
      -35                -30                -25
CCC ACT GTG GAC TCT GAG GCC TCT GCA TTT GTG GGT GGT CTG CCT GTG 374
Pro Thr Val Asp Ser Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val
      -20                -15                -10
ATA TTT TGG TCA TGG GCT GGT CTG GTC 401
Ile Phe Trp Ser Trp Ala Gly Leu Val
      -5                1
```

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..268
id HSC2SG081
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..181
id R13964
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 184..262
id R13964
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..230
id H0ML13589
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..136
id H05572
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..337
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 139..220
id H05572
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AACAGTTACG CGCCGCACGG ATC ATG GCC GCA GCC GCT CTG GGG CAG ATC TGG 53
Met Ala Ala Ala Ala Leu Gly Gln Ile Trp
-20 -15

GCA CGA AAG CTT CTC TCT GTC CCT TGG CTT CTG TGT GGT CCC AGA AGA 101
Ala Arg Lys Leu Leu Ser Val Pro Trp Leu Leu Cys Gly Pro Arg Arg
-10 -5 1

TAT GCC TCC TCC AGT TTC AAG GCT GCA GAC CTG CAG CTG GAA ATG ACA 149
Tyr Ala Ser Ser Ser Phe Lys Ala Ala Asp Leu Gln Leu Glu Met Thr
5 10 15 20

CAG AAG CCT CAT AAG AAG CCT GGC CCC GGC GAG CCC CTG GTG TTT GGG 197
Gln Lys Pro His Lys Lys Pro Gly Pro Gly Glu Pro Leu Val Phe Gly
25 30 35

AAG ACA TTT ACC GAC CAC ATG CTG ATG GTG GAA TGG AAT GAC AAG GGC 245
Lys Thr Phe Thr Asp His Met Leu Met Val Glu Trp Asn Asp Lys Gly
40 45 50

TGG GGC CAG CCC CGA ATC CAG CCC TTC CAG AAC CTC ACG CTG CAC CCA 293
Trp Gly Gln Pro Arg Ile Gln Pro Phe Gln Asn Leu Thr Leu His Pro
55 60 65

GCC TCC TCC AGC CTC CAC TAC TCC CTG CAG CTG TTT GAG GGC 335
Ala Ser Ser Ser Leu His Tyr Ser Leu Gln Leu Phe Glu Gly
70 75 80

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 50..169
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 219..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 213..338
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 2..336
id W79731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..326
id H21245
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 34..305
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 302..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 306..348
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 22..183
id W19587
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 201..284
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 183..266
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 283..344
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 266..327
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..161
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq CPLLLLVFTTNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

AAGGGGTCGG AGGTCAGGGC GAGCGTCTCG CAGGCCGTAG GAGGAAG ATG GCG GTG	56
Met Ala Val	
GAG TCG CGC GTT ACC CAG GAG GAA ATT AAG AAG GAG CCA GAG AAA CCG	104
Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro Glu Lys Pro	
-35 -30 -25 -20	
ATC GAC CGC GAG AAG ACA TGC CCA CTG TTG CTA CTG GTC TTC ACC ACC	152
Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Val Phe Thr Thr	
-15 -10 -5	
AAT AAC GGC CGC CAC CAC CGA ATG GAC GAG TTC TCC CGG GGA AAT GTA	200
Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg Gly Asn Val	
1 5 10	
CCG TCC AGC GAG TTG CAG ATC TAC ACT TGG ATG GAT GCA ACT TTG AAA	248
Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala Thr Leu Lys	
15 20 25	
GAA CTG ACA AGC TTA GTA AAA GAA GTC TAC CCA GAA GCT AGA WAG AAG	296
Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala Arg Xaa Lys	
30 35 40 45	
GGC ACT CAC TTC AAT TTT GCA VTC GTT TTT ACA GAT GTT AAA AGA CCT	344
Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val Lys Arg Pro	
50 55 60	

(2) INFORMATION FOR SEQ ID NO: 280:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 72..338
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 332..363
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..290
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 274..305
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 24..290
id H81957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 59..324
id W82998
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 64..329
id AA023811
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 240..305
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ACTAGCCTGC GAGTGTCTTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA    60
GTAGTGGAAA CGTTGCTTCT GAGGGGTGTC CAAGATGASC GGTTCAMCG GAGKTCAAGC   120
TGAACCAGCC ACCCGAGGAT GGCATCTCCT CCGTGAAGTT CAGCCCCAAC ACCTCCCACT    180
TCCTGCTTGT CTCCTCCTGG GACACGTCCG TCGTCTCTA CGATGTGCCG GCCAACTCC    239
ATG CGG CTC AAG TAC CAG CAC ACC GGC GCC GTC CTG GAC TGC GCC TTC    287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
   -20                      -15                      -10

TAC GAT CCA ACG CAT GCC TGG AGT GGA GGA CTA GAT CAT CAA TTG AAA    335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
   -5                      1                      5                      10

ATG CAT GAT TTG AAC ACT GAT CAA GAA AAT CTT GTT GGG ACC ATG ATG    383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
          15                      20                      25

CCC CTA TCA GAT GTG TTG    401
Pro Leu Ser Asp Val Leu
          30
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 72..257
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 33..75
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..34
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 75..260
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..78
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 39..159
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92

region 144..223
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..42
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 84..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 55..166
id W71083
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ATAGGCGCAA G ATG GCG CTG CTT TTT GCA CGT TCT TTG CGC TTG TGC CGC	50
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg	
-85 -80 -75	
TGG GGA GCC AAA CGA TTG GGA GTT GCC TCC ACA GAG GCC CAG AGA GGC	98
Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly	
-70 -65 -60	
GTC AGT TTC AAA CTG GMA GAA AAA ACC GCC CAC AGC AGC CTG GCA CTC	146
Val Ser Phe Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu	
-55 -50 -45	
TTC AGA GAT GAT ACG GGT GTC AAA TAT GGC TTG GTG GGA TTG GAG CCC	194
Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro	
-40 -35 -30	
ACC AAG GTG GCC TTG AAT GTG GAG CGC TTC CGG GAG TGG GCA GTG GTG	242
Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val	
-25 -20 -15 -10	
CTG GCA GAC ACA GCG GTC ACC AGT GGC AGA GGG	275
Leu Ala Asp Thr Ala Val Thr Ser Gly Arg Gly	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 232:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE.
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 77..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ILLGNVCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```

ATTCCCCCTT GGGCGGTGGT GGAGGTGGTA ACCGTGATAG TAGCAGCTCC GCGGGCAGCA    60
ACAGCGACTA CGAGGG ATG GCG GCG GCT GCA GCA GGA ACT SNA ACA TCC CAG    112
          Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln
                    -65                      -60

AGG TTT TTC CAG AGC TTC TCG GAT GCC CTA ATC GAC GAG GAC CCC CAG    160
Arg Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln
   -55                      -50                      -45

GCG GCG TTA GAG GAG CTG ACT AAG GCT TTG GAA CAG AAA CCA GAT GAT    208
Ala Ala Leu Glu Glu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp
   -40                      -35                      -30                      -25

GCA CAG TAT TAT TGT CAA AGA GCT TAT TGT CAC ATT CTT CTT GGG AAT    256
Ala Gln Tyr Tyr Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn
          -20                      -15                      -10

TAC TGT GTT GCT GTT GCT GAT GCA AAG AAG TCT CTA GAA CTC AAT CCA    304
Tyr Cys Val Ala Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro
          -5                      1                      5

AAT AAT TCC ACT GCT ATG CTG AGA AAA GGA ATA TGT GAA TAC CAT GAA    352
Asn Asn Ser Thr Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu
   10                      15                      20

AAA AAC TAT GCT GCT GCC CTA GAA ACT TTT TAC AGA AGG ACG GGG    397
Lys Asn Tyr Ala Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
   25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 283:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 79..380
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..55
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 82..363
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..58
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 46..337
id R52491
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 65..247
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..53
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..52
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 266..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 268..307
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 129..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 71..263
id AA084554
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 315..379
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 256..320
id AA084554
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 139..318
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```
AGTGGCCCGG ATGTTGGGTG CAGCTGCCAG ATCCGCTGAT CTAGTGCTTC TCGAAAAAAA   60
CCTTCAGGCG GCCCATGGCT GTCGATATTC AACCAGCATG CCTTGGACTT TATTSYGGGA   120
AGACCCTATT ATTTAAAA ATG GCT CAA CTG AAA TAT ATG GAG AAT GTG GGG   171
          Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly
          -60              -55              -50
TAT GCC CAA GAG GAC AGA GGA CGA ATG CAC AGA AAT ATT GTC AGC CTT   219
Tyr Ala Gln Glu Asp Arg Glu Arg Met His Arg Asn Ile Val Ser Leu
          -45              -40              -35
GCA CAG AAT CTC CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG   267
Ala Gln Asn Leu Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp
          -30              -25              -20
```

```

CAA TGC TTC CTC TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG      315
Gln Cys Phe Leu Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg
      -15                      -10                      -5

GGA AAA AGA GTT CCA GCG CAC TTT TCC AAC ACA TCA CTG CAT TAT TTG      363
Gly Lys Arg Val Pro Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu
      1                      5                      10                      15

AAT GCA GCA TGG CCG CGG                                              381
Asn Ala Ala Trp Pro Arg
      20

```

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..292
id HUM524F053
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 48..176
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..279
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..43
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 16..50
id H81799
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 57..181
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 175..234
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..45
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..51
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 101..228
id W81213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..107
id W81213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 8..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..165
id AA090080
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..210

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 159..202
 id AA090080
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 174..266
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq WSPLSTRSGGTHA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AAAAACAATA GGACGGAAAC GCCGAGGAAC CCGGCTGAGG CGGCAGAGCA TCCTGGCCAG   60
AACAAGCCAA GGAGCCAAGA CGAGAGGGAC ACACGGACAA ACAACAGACA GAAGACGTAC   120
TGGCCGCTGG ACTCCKCTGC CTCCCCATC TCCCCGCCAT CTGCGCCCGG AGG ATG       176
                                     Met
AGC CCA GCC TTC AGG GCC ATG GAT GTG GAG CCC CGC GCC AAA GGS TCC       224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                -25                -20                -15

TTC TGG AGC CCT TTG TCC ACC AGG TCG GGG GGC ACT CAT GCG TGC TCC       272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
          -10                -5                1

GCT TCA ATG AGA CAA CCC TGG                                           293
Ala Ser Met Arg Gln Pro Trp
          5

```

(x) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 26..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 42..342
 id R71425
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 11..337
id AA133412
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..345)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 172..403
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(71..114)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 402..445
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(26..76)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 439..489
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 186..359
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 83..182
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..76
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 33..88
id W07240
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..307
id R81019
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 18..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SILAQVLDQSARA/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AGCGCTGACG CCGAGCC ATG GCG GAC GAG GAG CTT GAG GCG CTG AGG AGA      50
      Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg
                        -50                      -45

CAG AGG CTG GCC GAG CTG CAG GCC AAA CAC GGG GAT CCT GGT GAT GCG      98
Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala
      -40                      -35                      -30

GCC CAA CAG GAA GCA AAG CAC AGG GAA GCA GAA ATG AGA AAC AGT ATC      146
Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile
      -25                      -20                      -15

TTA GCC CAA GTT CTG GAT CAG TCG GCC CGG GCC AGG TTA AGT AAC TTA      194
Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu
      -10                      -5                      1                      5

GCA CTT GTA AAG CCT GAA AAA ACT AAA GCA GTA GAG AAT TAC CTT ATA      242
Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile
      10                      15                      20

CAG ATG GCA AGA TAT GGA CAA CTA AGT GAG AAG GTA TCA GAA CAA GGT      290
Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly
      25                      30                      35

TTA ATA GAR ATC CTT AAA AAA GTA AGC CAA CAA ACA GAA AAG AHN ACA      338
Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr
      40                      45                      50

ACA GTG AGG      347
Thr Val Arg
      55

```

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 186..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 156..352
 id AA082259
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 61..146
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 34..119
 id AA082259
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 29..61
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..33
 id AA082259
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 194..331
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 169..306
 id H80945
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 54..146
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 30..122
 id H80945
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 157..345
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq GLVCAGLADMARPAE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AACAGCGGGC AGGGAAAGCC GCGGGAAGGG TACTCCAGGC GAGAGGCGGA CGCGAGTCGT    60
CGTGGCAGGA AAAGTACTA GCTCCCCTTC GTTGTACAGC AGGGACGAGA ACACAGCCAC    120
GCTCCCAMCC GGCTGCCHAA GRWTCCTSG GCGGCG ATG TCG GCC GCC GGT GCC    174
                               Met Ser Ala Ala Gly Ala
                               -60

CGA GGC CTG CGG GCC ACC TAC CAC CGG CTC CTC GAT AAA GTG GAG CTG    222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
   -55                               -50                               -45

ATG CTG CCC GAG AAA TTG AGG CCG TTG TAC AAC CAT CCA GCA GGT CCC    270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
   -40                               -35                               -30

AGA ACA GTT TTC TTC TGG GCT CCA ATT ATG AAA TGG GGG TTG GTG TGT    318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
   -25                               -20                               -15                               -10

GCT GGA TTG GCT GAT ATG GCC AGA CCT GCA GAA AAA CTT AGC ACA GCT    366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
           -5                               1                               5

CAA TCT GVK GTT TTG ATG GCT ACA GGG TTT ATT TGG TCA AGA TAC TCG    414
Gln Ser Xaa Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
    10                               15                               20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 185..380
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 46..192
id W07314

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 409..478
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 401..470
id W07314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..412
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 12..390
id W07582
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..393
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 31..379
id W73850
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..52
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..37
id W73850
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..447
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..375
id AA112776
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..388
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..326
id H72671
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 98..355
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5

seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 287:

```

AACTTGTCAG CCCTGTCTG AGGCGGAGGC AGCCCCGCGC CGCGCCGGAC CCGAGCATAT      60
TTCATTTTCT GTCATTGGAC TTTGAGCCAT TAGAACC ATG AGC AAC TAC AGT GTG      115
                               Met Ser Asn Tyr Ser Val
                               -85
TCA CTG GTT GGC CCA GCT CCT TGG GGT TTC CGG CTG CAG GGC GGT AAG      163
Ser Leu Val Gly Pro Ala Pro Trp Gly Phe Arg Leu Gln Gly Gly Lys
-80                -75                -70                -65
GAT TTC AAC ATG CCT CTG ACA ATC TCT AGT CTA AAA GAT GGC GGC AAG      211
Asp Phe Asn Met Pro Leu Thr Ile Ser Ser Leu Lys Asp Gly Gly Lys
                -60                -55                -50
GCA GCC CAG GCA AAT GTA AGA ATA GGC GAT GTG GTT CTC AGC ATT GAT      259
Ala Ala Gln Ala Asn Val Arg Ile Gly Asp Val Val Leu Ser Ile Asp
                -45                -40                -35
GGA ATA AAT GCA CAA GGA ATG ACT CAT CTT GAA GCC CAG AAT AAG ATT      307
Gly Ile Asn Ala Gln Gly Met Thr His Leu Glu Ala Gln Asn Lys Ile
                -30                -25                -20
AAG GGT TGT ACA GGA NYT TTG AAT ATG ACT CTG CAA AGA GCA TCT GCT      355
Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr Leu Gln Arg Ala Ser Ala
                -15                -10                -5
GCA CCC AAG CCT GAG CCG GTT CCT GTT CAA AAG CCC ACA GTC ACC AGC      403
Ala Pro Lys Pro Glu Pro Val Pro Val Gln Lys Pro Thr Val Thr Ser
    1                5                10                15
GTG TGT TCC GAG ACT TCT CAG GAG CTA GCA GAG GGA CAG AGA AGA GGA      451
Val Cys Ser Glu Thr Ser Gln Glu Leu Ala Glu Gly Gln Arg Arg Gly
                20                25                30
TCC CAG GGT GAC AGT AAA CAG CAA AAT      478
Ser Gln Gly Asp Ser Lys Gln Gln Asn
                35                40

```

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (B) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 4..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..330
id N35568
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..297
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..272
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 295..338
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 271..314
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..212
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 209..313
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 13..320
id HSC1MA011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..339
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..278
id R61491
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 245..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEaIG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

ATTCGTTTAC AGTTCGGCAC GTAGGACGGA GGGTAGTGCG TCTAGAGACA CATATTCCCA   60
ACGGATTTGA CGATGGTGTT CGGTCTTGAA TGGAAATGTA GTCTTAGGCC AGTCTTAGGT  120
TTTGAACAG GATAGTAGGT ATCCGGAGTC GATTGAGGGC CAGAGCAGGC ACTGGGGTTC  180
GGATCCTGGG CAAAGTTTCC CACATTGAGG GTCTCGAGGA CGCCTAGATC TCTTTCCAG   240
GGCC ATG GCG AAC CCG AAG CTG CTG GGA CTG GAG CTA AGC GAG GCG GAG   289
    Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
        -15          -10          -5

GCG ATC GGT GCT GAT TCG GCG CGA TTT GAG GAG CTG CTG CTG CAG GCC   337
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
        1              5              10

TCG AAG GAG CTC CAG CAA                                           355
Ser Lys Glu Leu Gln Gln
    15

```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 90..178
id W21193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 2..53
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..89
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 269..345
id AA058174
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 204..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALLCTLLHLHFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```
AAAGGTGTCT GGATCGGAGG GAGGTTGGGG TGGGCATCGG GCGGCTGGAA GAGCTCGACT   60
CGTCCCGGCTG GGAAGCGCG AGTCTGAGTG GAACCCTGGA CGACTTGCAG AGCGGCTGGC   120
GCAGTCATGG CGGACTACTG GAAGTCACAG CCAAAGAAAT TCTGTGATTA CTGCAAGTGC   180
TGSATAGCAG ACAATAGGCC TGT ATG ATA ATT CCG CTG TTA GAG ATT CTA ATA   233
      Met Ile Ile Pro Leu Leu Glu Ile Leu Ile
      -40                               -35
ATA ATT TTT TTG AAT GAA GTG CTC CTT TTT GAT GTA AAC TCA GTT TAC   281
```

```

Ile Ile Val Leu Asn Glu Val Leu Leu Phe Asp Val Asn Ser Val Tyr
-30                      -25                      -20                      -15

AAA GCA CTT TTA TGT ACA TTG CTC TTG CAT TTT CAA AAC ATC AGA AGA      329
Lys Ala Leu Leu Cys Thr Leu Leu Leu His Phe Gln Asn Ile Arg Arg
      -10                      -5                      1

TTT CTG TCT TCT CAG TCC CCT ATG AAA GCT GTG AGC CTT CTA THT TTT      377
Phe Leu Ser Ser Gln Ser Pro Met Lys Ala Val Ser Leu Leu Xaa Phe
      5                      10                      15

CAT CAA CCT GAC TTT GAT TAT ATA
His Gln Pro Asp Phe Asp Tyr Ile      401
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..382
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 97
region 4..337
id HUMGPCRB
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..54
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 345..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 55..92
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..235

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.4
 seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AACTTCAGTT TGGACAAC TA CTCACAGCTA CTACACAGAG ACCCGAACGA GTCAGTGATA   60
TACACCTGGA CCACCACCA ATG GAT ATA CAA ATG GCA AAC AAT TTT ACT CCG   112
      Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro
      -50                               -45

CCC TCT GCA ACT CCT CAG GGA AAT GAC TGT GAC CTC TAT GCA CAT CAC   160
Pro Ser Ala Thr Pro Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His
  -40                -35                -30

AGC ACG GCC AGG ATA GTA ATG CCT CTG CAT TAC AGC CTC GTC TTC ATC   208
Ser Thr Ala Arg Ile Val Met Pro Leu His Tyr Ser Leu Val Phe Ile
  -25                -20                -15                -10

ATT GGG CTC GTG GGA AAC TTA CTA GCC TTG GTC GTC ATT GTT CAA AAC   256
Ile Gly Leu Val Gly Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn
      -5                1                5

AGG AAA AAA ATC AAC TCT ACC ACC CTC TAT TCA ACA AAT TTG GTT ATT   304
Arg Lys Lys Ile Asn Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile
      10                15                20

TCT GAT ATA CTT TTT ACC ACC GCT TTG CCT ACA CGA ATA GCT ACT ATG   352
Ser Asp Ile Leu Phe Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met
      25                30                35

CMA TGG GCY TTG ACT GGA GAA TCG GAG ATG TGG   385
Xaa Trp Ala Leu Thr Gly Glu Ser Glu Met Trp
      40                45                50
  
```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (E) TISSUE TYPE: Pancreas

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 55..462
 (C) IDENTIFICATION METHOD: fasta
 (D) OTHER INFORMATION: identity 99
 region 1..408
 id HUMORF06
 vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..218
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 216..365
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 412..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 366..416
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..409
id C16991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 212..411
id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 52..214
id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..58

id N28784
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..303
id C17735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 303..408
id C17735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 47..209
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 263..406
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 207..350
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 406..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..407
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..53
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 357..443
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AGTTCGTTTA TTCCTCCGCG CGCTGGGACA GGCTGCTTCT TCGCCAGAAC CAACCGGTTG   60
CTTGCTGTCC CAGCGGCGCC CCCTCATCAC CGTCGCCATG CCCGGAGGTC TGCTTCTCGG   120
GGACGTGGCT CCCAACTTTG AGGCCAATAC CACCGTCGGC CGCATCCGTT TCCACGACTT   180
TCTGGGAKAC TCATGGGGCA TTCTCTTCTC CCACCCTCGG GACTTTACCC CASTGTGCAC   240
CACAGAGCTT GGCAGAGCTG CAAAGCTGGC ACCAGAATTT GCCAAGAGGA ATGTTAAGTT   300
GWTTGCCCTT TCAATAGACA GTGTTGAGGA CCATCTTGCC TGGAGCAAGG ATATCA ATG   359
                                         Met

CTT ACA ATT GTG AAG AGC CCA CAG AAA AGT TAC CTT TTC CCA TCA TCG   407
Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser Ser
      -25                -20                -15

ATG ATA GGA ATC GGG AGC TTG CCA TCC TGT TGG GCA TGC TGG ATC CAG   455
Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile Gln
      -10                -5                1

CAG AGA                                         461
Gln Arg
5

```

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15
seq LFLLLLLAASAWG/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```

Met Ser Ser Trp Ser Arg Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln
-35                -30                -25                -20

Pro His Val Ser Arg Thr Leu Phe Leu Leu Leu Leu Ala Ala Ser
      -15                -10                -5

```

Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser
 1 5 10
 Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly
 15 20 25
 Tyr Leu Pro Ala Thr
 30

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.2
seq LLLXAVLLSLASA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Xaa Ala Val Leu Leu
 -20 -15 -10
 Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 -5 1 5 10
 Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 15 20 25
 Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
 30 35 40
 Glu Ser Glu Leu Glu Xaa Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys
 45 50 55
 Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser
 60 65 70 75

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.1
seq CVLLLLLLLLLTRS/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
-20 -15 -10
Leu Leu Thr Arg Ser Ser Glu Val Glu Xaa Xaa Ala Glu Val Gly Gln
-5 1 5 10
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
15 20 25
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
30 35 40
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
45 50 55
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
60 65 70 75
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
80 85 90
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu
95 100

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLFLFLAVDEAWA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala Val
-20 -15 -10

Asp Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Gly Arg
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq SLLLAVALGLATA/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Lys Ser Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Ala Thr
-15 -10 -5

Ala Val Ser Ala Gly Pro Ala Val Ile Glu Cys Trp Phe Val Glu Asp
1 5 10 15

Ala Ser Gly Lys Gly Leu Ala Lys Arg Pro Gly Ala Leu Leu Leu Arg
20 25 30

Gln Gly Pro Gly Glu Pro Pro Pro Arg Pro Asp Leu Asp Pro Glu Leu
35 40 45

Tyr Leu Ser Val His Asp Pro Ala Gly Ala Leu Gln Ala Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.6

seq LLTLXLLGGPTWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Leu Leu Leu Leu Thr Leu Xaa Leu Leu Gly Gly Pro Thr Trp Ala
-15 -10 -5

Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu
1 5 10 15

Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu
20 25 30

Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys
35 40 45

Leu Gly Ala Leu Xaa Gly Asn Thr Gln Glu Val Xaa Xaa Gln Pro Gly
50 55 60

Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly
65 70 75 80

Met Val Met Tyr Thr Ser Lys Asp Arg
85

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.4

seq LIILIXIWIWCLG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

Met Lys Ile Gly Ile Leu Leu Ser Leu Leu Asn Ser Val Ile Ser Gln
-45                      -40                      -35

Thr Leu Met Ser Cys Asn Trp Lys Gln Gln Met Arg Arg Met Lys Thr
-30                      -25                      -20                      -15

Ile Leu Ile Ile Leu Ile Xaa Ile Trp Ile Trp Cys Leu Gly Ser Gln
                      -10                      -5                      1

Thr Phe Gly Thr Ser Thr Thr Lys Ser Val Gln Leu Lys Ile Leu Arg
      5                      10                      15

Gln Asn Leu Ser His Phe Leu Gln Pro Pro Gln Val Ile
  20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.4
seq LPFLLSLFPGALP/VQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

Met Lys Ala Ser Ser Gly Arg Cys Gly Leu Val Arg Trp Leu Gln Val
-30                      -25                      -20                      -15

Leu Leu Pro Phe Leu Leu Ser Leu Phe Pro Gly Ala Leu Pro Val Gln
      -10                      -5                      1

Ile Arg Tyr Ser Ile Pro Glu Glu Leu Ala Lys Asn Ser Val Val Gly
      5                      10                      15

Asn Leu Ala Lys Asp Leu Gly Leu Ser Val Arg Asp Leu Pro Ala Arg
  20                      25                      30

Lys Leu Arg Val Ser Ala Glu Lys Glu Tyr Phe Thr Val Asn Pro Glu
  35                      40                      45                      50

Ser Gly Asp Leu Leu Val Ser Asp Arg Ile Asp Arg Asp Val
      55                      60

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq IIFLCHLLRGLHA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ile Val Asp Cys Val Ser Ser His Leu Lys Lys Thr Gly Asp Gly
-30 -25 -20

Ala Lys Thr Phe Ile Ile Phe Leu Cys His Leu Leu Arg Gly Leu His
-15 -10 -5

Ala Xaa Thr Asp Arg Glu Lys Asp Pro Leu Met Cys Glu Asn Ile Gln
1 5 10 15

Thr His Gly Arg Leu Pro
20

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -104..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq LTSLSWLLXASCS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Ala Lys Ala Leu Leu Phe Pro Ser Gly Arg Ser Val Arg Val Leu

-100 -95 -90
 Tyr Gly Ala Val Asn Lys Glu Arg Gln Xaa Glu Ser Val Leu Asn Arg
 -85 -80 -75
 Ala Cys Pro Pro Lys Ala Asn Ser Lys Glu Arg Arg Gly Arg Ala Val
 -70 -65 -60
 Leu Gly Ala Glu Leu Thr Gln Trp Ser Ser Pro Thr Thr Ala Gly Ser
 -55 -50 -45
 Cys Cys Ser Ser Cys Thr Leu Cys Ala Arg Ser Ser Ser Xaa Val Ile
 -40 -35 -30 -25
 Ala Pro Ser Pro Leu Val Pro Phe Thr Ser Gly Leu Thr Ser Leu Ser
 -20 -15 -10
 Trp Leu Leu Xaa Ala Ser Cys Ser Lys Pro Xaa Lys Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq LATKLSSLSGVFA/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
 -70 -65 -60
 Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
 -55 -50 -45
 Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala
 -40 -35 -30
 Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
 -25 -20 -15 -10
 Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
 -5 1 5
 Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu

```

      10          15          20
Ala Gly Met Pro Ser Pro Glu Trp Thr Xaa Arg Lys Lys Gln Thr Xaa
    25              30              35
Glu Asn Trp Ala Trp Arg Asp Ser Arg Gln Arg Xaa Arg Gly Val Leu
    40              45              50              55
Val Val Gly Ile Gly Ala
           60
```

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(v) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
 seq VLVLLISFFTFDGDG/HG
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp  
-15 -10 -5

Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu  
1 5 10 15

Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Met  
20 25

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: S adrenals

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq WIFLAAILKGVQC/EV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly  
                  -15                  -10                  -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys  
                  1                  5                  10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe  
          15                  20                  25

Thr Asp Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
          30                  35                  40                  45

Glu Trp Val Ala Asn Ile Xaa Ser Thr Ala Ser Gly Gly Thr Arg Gly  
                  50                  55                  60

Tyr Ala Ala Pro Val Lys Asp Arg Phe Ile Ile Ser Arg Asp Asp Ser  
          65                  70                  75

Arg Asn Thr Leu His Leu Gln Met Asn Gly Leu Lys Xaa Met Thr Gln  
          80                  85                  90

Ala Ile Tyr Tyr Cys Ala Thr  
          95                  100

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LWRLLLWAGTAFQ/VX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Met Ala Glu Pro Gly His Ser His His Leu Ser Ala Arg Val Arg Gly  
          -35                  -30                  -25

Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala  
 -20 -15 -10  
 Gly Thr Ala Phe Gln Val Xaa Gln Gly Xaa Xaa Pro Glu Leu Xaa Ala  
 -5 1 5 10  
 Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr  
 15 20 25  
 Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Xaa Gly Leu Cys Thr  
 30 35 40  
 Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Xaa Xaa Ser Cys Asn  
 45 50 55  
 Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Xaa Pro Cys Ala  
 60 65 70 75  
 Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp  
 80 85 90  
 Glu Leu Pro His Gly Phe Ala Ala Ser Gln Pro Thr Trp Ser Trp Met  
 95 100 105  
 Thr Val Leu Leu Ser His  
 110

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq QACLLGLFALILS/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Met Thr Ala Asp Pro Arg Lys Gly Arg Met Gly Leu Gln Ala Cys Leu  
 -25 -20 -15 -10  
 Leu Gly Leu Phe Ala Leu Ile Leu Ser Gly Lys Cys Ser Xaa Ser Pro  
 -5 1 5  
 Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp Val Ser Leu Gly  
 10 15 20



Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln  
 25 30 35  
 Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro  
 40 45 50 55  
 Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp  
 60 65 70  
 Leu Val Arg Pro Ser Pro Leu Thr Pro  
 75 80

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq LCFLLLAVAMSFF/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu  
 -20 -15 -10  
 Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu  
 -5 1 5  
 Thr Arg Ala His Leu Leu Leu Lys Xaa Lys Met Met Arg Leu Gly Gly  
 10 15 20  
 Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met  
 25 30 35 40  
 Thr Leu Xaa Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe  
 45 50 55  
 Pro Pro Ser Met His Phe Phe  
 60

## (2) INFORMATION FOR SEQ ID NO: 308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq LVLVLVVAVTVRA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ala | Pro | Leu | Val | Leu | Val | Leu | Val | Val | Ala | Val | Thr | Val | Arg |  |
|     | -15 |     |     |     |     | -10 |     |     |     |     |     |     | -5  |     |     |  |
| Ala | Ala | Leu | Phe | Arg | Ser | Ser | Leu | Ala | Glu | Phe | Ile | Ser | Glu | Arg | Val |  |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Glu | Val | Val | Ser | Pro | Leu | Ser | Ser | Trp | Lys | Arg | Val | Val | Glu | Gly | Leu |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |  |
| Ser | Leu | Leu | Asp | Leu | Gly | Val | Ser | Pro | Tyr | Ser | Gly | Ala | Val | Phe | His |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Glu | Thr | Pro | Leu | Ile | Ile | Tyr | Leu | Phe | His | Phe | Leu | Ile | Asp | Tyr | Ala |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     |     | 60  |     |     |  |
| Glu | Leu | Val | Phe | Met | Ile | Thr | Asp | Ala | Leu | Thr | Ala | Ile | Ala | Leu | Tyr |  |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |  |
| Phe | Ala | Ile | Gln | Asp | Phe | Asn | Lys | Val | Val | Phe | Lys | Lys | Gln | Lys | Leu |  |
|     | 80  |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |  |
| Leu | Leu | Glu | Leu | Asp | Gln | Tyr | Ala | Pro | Asp | Val | Ala | Glu | Leu | Ile | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     | 110 |  |

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -102..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
 seq LXMTLMLPFKILS/DS "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

```

Met Thr Ala Ala Ile Arg Arg Gln Arg Glu Leu Ser Ile Leu Pro Lys
 -100 -95 -90

Val Thr Leu Glu Ala Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg
 -85 -80 -75

Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro
 -70 -65 -60 -55

Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu
 -50 -45 -40

Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile
 -35 -30 -25

Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Xaa Met Thr Leu Met Leu
 -20 -15 -10

Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg
 -5 1 5 10

Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr
 15 20 25

Val Gly Glu Gly
 30

```

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Spleen

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -46..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq SIGVLTLSHLISG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Ser Ser Val Leu Ala Ala Ser His Pro Leu Val Leu Ser Ser Asn

```

-45                      -40                      -35  
 Ala Gly Thr Pro Gly Ile Ser Glu Lys Asp Asn Arg Asp Pro Ala Gly  
 -30                      -25                      -20                      -15  
 Ser Ser Ile Gly Val Leu Thr Leu Ser His Leu Ile Ser Gly Leu Arg  
                     -10                      -5                      1  
 Thr Leu Tyr Thr Leu Leu His Phe Pro Leu Arg  
                     5                      10

## (2) INFORMATION FOR SEQ ID NO: 311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq LIILGLVLFMVYGV/NV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly  
 -50                      -45                      -40                      -35  
 Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val  
                     -30                      -25                      -20  
 Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val  
                     -15                      -10                      -5  
 Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu  
                     1                      5                      10  
 Arg Arg Ala Glu Gly Leu Tyr Xaa Gln Leu Leu Gly Leu Thr Ala Ser  
                     15                      20                      25                      30  
 Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp  
                     35                      40                      45  
 Ala Ile Met Gln Met Trp Leu Asn Ala  
                     50                      55

## (1) INFORMATION FOR SEQ ID NO: 312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq SCLVSGWGLLANG/QR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
                  -60                  -55                  -50

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
                  -45                  -40                  -35

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
                  -30                  -25                  -20

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
                  -15                  -10                  -5

Gln Arg  
1

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq VICCVLFLLFILG/YI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```
Met Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro
-45 -40 -35
```

---

```
Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
-30 -25 -20
```

---

```
Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr
-15 -10 -5 1
```

---

```
Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val
5 10 15
```

---

```
Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn
20 25 30
```

---

```
Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu
35 40 45
```

---

```
Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr
50 55 60 65
```

---

```
Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Xaa Xaa
70 75 80
```

---

```
Lys Thr Ser Ser His Arg Leu Leu Gly Lys Ser Ser Ile Gln
85 90 95
```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq VLLFLAWVCFLEY/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe Leu  
-15 -10 -5

Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu Thr Arg  
1 5 10

Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro Gly Pro Gly  
15 20 25 30

Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala Cys Trp Met Ala  
                   35                  40                  45

Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile Asp Ala Leu Arg Phe  
                   50                  55                  60

Asp Phe Ala Gln Pro Gln His Ser His Val Pro Arg Glu Pro Pro Val  
                   65                  70                  75

Ser Leu Pro Phe Leu Gly Lys Leu Ser Ser Leu Gln Arg Ile Leu Glu  
                   80                  85                  90

Ile Gln Pro His His Ala Arg Leu  
                   95                  100

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq CWMMLLGSGXGSFL/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Ser Pro Val Leu His Phe Tyr Val Arg Pro Ser Gly His Glu Gly  
   -80                  -75                  -70

Ala Ala Ser Gly His Thr Arg Arg Lys Leu Gln Gly Lys Leu Pro Glu  
  -65                  -60                  -55                  -50

Leu Gln Gly Val Glu Thr Glu Leu Cys Tyr Asn Val Asn Trp Thr Ala  
                   -45                  -40                  -35

Glu Ala Leu Pro Ser Ala Glu Glu Thr Lys Lys Leu Met Trp Leu Phe  
                   -30                  -25                  -20

Gly Cys Pro Tyr Cys Trp Met Met Leu Leu Gly Ser Xaa Gly Ser Phe  
                   -15                  -10                  -5

Leu Ala Pro Met Thr Cys Xaa Trp Arg Ser  
   1                  5

## (2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Brain
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -36..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.6  
                            seq ILRLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```
Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
 -35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
 -20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
 1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
 15 20 25

Pro Ser Asn Met Tyr Thr Lys Tyr Tyr Ile His Arg Asn Gly
 30 35 40
```

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -21..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.6  
                            seq LLRVNLPHNSIG/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:



Met Met Gly Val Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro  
 -20 -15 -10  
 His Asn Ser Ile Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu  
 -5 1 5 10  
 Glu Trp Leu Asn Leu Ala Gly Asn Asn Leu Lys Ala Met Glu Gln Xaa  
 15 20 25  
 Asn Ser Cys Thr Ala Leu Gln His Leu Asp  
 30 35

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq ILRLLGSLSNAYS/PR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly  
 -35 -30 -25  
 Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser  
 -20 -15 -10 -5  
 Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met  
 1 5 10  
 Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp  
 15 20 25  
 Arg

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Colon

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -13..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```
Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
 -10 -5 1
Ala Ala Ser Met Gln Glu Glu Val Arg Thr Ala Pro Arg Ala Leu
 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -47..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq GCGMFTFLSSVXA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```
Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
 -45 -40 -35
Gly Thr Ala Val Glu Thr Glu Gly Xaa Gly Ser Arg His Pro Pro Trp
 -30 -25 -20
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Xaa Ala Ala
 -15 -10 -5 1
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
 5 10 15
Leu Leu Gln Ile Lys Thr Leu Leu Ala Xaa Ser Cys His Glu Gln Glu
```

20 25 30  
Met Val Val Ser Ser Leu Val Ile Gly .  
35 40

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LLFPVGRSWSCFA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Glu Thr Phe Leu Glu Pro Asn Asn Lys Lys Leu Leu Phe Pro Val  
-20 -15 -10  
Gly Arg Ser Trp Ser Cys Phe Ala Gln Thr Xaa Ser Leu Ala Lys Tyr  
-5 1 5  
Ile Pro Tyr Ser Leu Trp Lys Tyr Ser Val Leu Ser Gly His Ser  
10 15 20

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq FLWGLALPLFFFC/WE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

|                                                                 |     |    |
|-----------------------------------------------------------------|-----|----|
| Met Gly Phe Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys Trp |     |    |
| -15                                                             | -10 | -5 |
|                                                                 |     | 1  |
| Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala |     |    |
| 5                                                               | 10  | 15 |
| Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu |     |    |
| 20                                                              | 25  | 30 |
| Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr |     |    |
| 35                                                              | 40  | 45 |
| Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Val Pro Glu Ala Glu Thr |     |    |
| 50                                                              | 55  | 60 |
| Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr |     |    |
| 70                                                              | 75  | 80 |
| Lys Thr Xaa Pro Asn Phe Met Val Leu Xaa Xaa Xaa Val Thr         |     |    |
| 85                                                              | 90  | 95 |

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq WLLSDILGQGATA/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ser | Thr | Ser | Asn | His | Leu | Trp | Leu | Leu | Ser | Asp | Ile | Leu | Gly |
|     | -20 |     |     |     |     | -15 |     |     |     |     |     | -10 |     |     |     |
| Gln | Gly | Ala | Thr | Ala | Asn | Val | Phe | Arg | Gly | Arg | His | Lys | Lys | Thr | Gly |
|     | -5  |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| Asp | Leu | Phe | Ala | Ile | Lys | Val | Phe | Asn | Asn | Ile | Ser | Phe | Leu | Arg | Pro |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| Val | Asp | Val | Gln | Met | Arg | Glu | Phe | Glu | Val | Leu | Lys | Lys | Leu | Asn | His |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |

Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Gly  
45 50 55

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq ICAGSVLPPYSNC/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Val Glu Ile Cys Ala Gly Ser Val Leu Pro Pro Tyr Ser Asn Cys  
-15 -10 -5

Gln Met Pro Glu Pro Ser Ile Phe Thr Leu Ile His Phe His Thr Tyr  
1 5 10 15

Tyr Cys Leu Thr Thr Pro Gln  
20

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LLAFGTSCSVVXY/XP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn  
                   -40                  -35                  -30

Arg Val Arg Gly Val Leu Asn Trp Xaa Ser Gly Pro Arg Gly Leu Leu  
                   -25                  -20                  -15

Ala Phe Gly Thr Ser Cys Ser Val Val Xaa Tyr Xaa Pro Leu Xaa Arg  
                   -10                  -5                  1                  5

Val Val Val Thr Xaa Leu Xaa Gly His Thr Ala Arg Val Asn Cys Ile  
                   10                  15                  20

Gln Trp Ile Xaa Lys Gln Xaa Gly Met  
                   25                  30

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -70...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq QLLLATLQEAATT/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala  
                   -70                  -65                  -60                  -55

Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu  
                   -50                  -45                  -40

Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg  
                   -35                  -30                  -25

Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu  
                   -20                  -15                  -10

Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp  
                   -5                  1                  5                  10

Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly  
                   15                  20                  25

Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg  
                   30                  35                  40

Gln Leu Ser Pro Ser  
45

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LLPFGMLCASSTT/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

```

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro
-25 -20 -15

Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His
-10 -5 1 5

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
10 15 20

Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
25 30 35

Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
40 45 50

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu
55 60 65

```

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -110..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq HTXGLLGFRXQG/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

```

Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
-110 -105 -100 -95

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
 -90 -85 -80

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
 -75 -70 -65

Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
 -60 -55 -50

Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
-45 -40 -35

Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Xaa Ala Arg Arg Thr
-30 -25 -20 -15

Leu His Thr Xaa Gly Leu Leu Gly Phe Gly Arg Xaa Gln Gly Ser Ile
 -10 -5 1

Pro Lys Gly Pro Glu Gly Leu Xaa Asp Glu Phe Val Xaa Ser Ile Xaa
5 10 15

Thr Trp Arg Glu Thr Trp
20

```

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Large intestine

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq PLSMILLSDKIQS/SK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:





## (2) INFORMATION FOR SEQ ID NO: 331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq STCCWCTPGGAST/ID

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Ser Thr Cys Cys Trp Cys Thr Pro Gly Gly Ala Ser Thr Ile Asp  
                  -10                  -5                  1  
Phe Leu Lys Arg Tyr Ala Ser Asn Thr Pro Ser Gly Glu Phe Gln Thr  
          5                  10                  15  
Ala Asp Glu Asp Leu Cys Tyr Cys Leu Gly  
      20                  25

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VVEILPYLPCLTA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

Ala Leu Ile Xaa Leu  
10

## (2) INFORMATION FOR SEQ ID NO: 334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LLXCVGNFFGSTQ/DA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Ala Gln Lys Pro Leu Arg Leu Leu Ala Cys Gly Asp Val Glu Gly
 -45 -40 -35

Lys Phe Asp Ile Leu Phe Asn Arg Val Gln Ala Ile Gln Lys Xaa Ser
 -30 -25 -20

Gly Asn Phe Asp Leu Leu Xaa Cys Val Gly Asn Phe Phe Gly Ser Thr
 -15 -10 -5

Gln Asp Ala Glu Trp Glu Glu Tyr Lys Thr Gly Ile Lys Lys Ala Pro
 1 5 10 15

Ile Gln Thr Tyr Val Leu Gly Ala Asn Asn Gln Glu Thr Val Lys Tyr
 20 25 30

Phe Gln Asp Ala Asp Gly Cys Glu Leu Ala Glu Asn Ile Thr Tyr Leu
 35 40 45

Gly Arg Gly
 50

```

## (2) INFORMATION FOR SEQ ID NO: 335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -52..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.8  
 seq RPVLLHLHQTAAH/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
 -50 -45 -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
 -35 -30 -25

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
 -20 -15 -10 -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
 1 5 10

Gln Gln Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
 15 20 25

Ile Ala Xaa Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Xaa His
 30 35 40

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile
 45 50 55

```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Testis

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -52..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.8  
 seq RPVLLHLHQTAAH/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Xaa Trp Lys Met
 -50 -45 -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
 -35 -30 -25

```

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
 -20 -15 -10 -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
 1 5 10

Gln Gly

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser  
 -35 -30 -25

Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala  
 -20 -15 -10 -5

Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln  
 1 5 10

Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro  
 15 20 25

Gln Xaa Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val  
 30 35 40

Glu Lys Asn Lys Tyr Asp Ala Thr Gly  
 45 50

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -58..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LVSFVAVSSEGTEQ/GE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Arg Asp Cys Pro Gly Val Glu Xaa Ile Leu Asp Cys Ser Xaa Arg  
-55 -50 -45

Gln Lys Thr Glu Gly Cys Arg Leu Gln Ala Gly Lys Glu Cys Val Asp  
-40 -35 -30

Ser Pro Val Glu Gly Gly Gln Ser Glu Ala Pro Pro Ser Leu Val Ser  
-25 -20 -15

Phe Ala Val Ser Ser Glu Gly Thr Glu Gln Gly Glu Asp Pro Arg Ser  
-10 -5 1 5

Glu Lys Asp His Ser Arg Pro His Lys His Arg Ala Arg His Ala Arg  
10 15 20

Leu Arg Arg Ser Glu Ser Leu Ser Xaa Lys Gln Val Lys Glu Ala Lys  
25 30 35

Ser Xaa Cys Lys Ser Ile Ala Leu Leu Leu Thr Asp Ala Pro Xaa Pro  
40 45 50

Asn Ser Lys Gly Val Leu Met Phe Lys Lys Arg  
55 60 65

## (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LVFNFLILITILT/IW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
 -35 -30 -25

Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
 -20 -15 -10

Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
 -5 1 5 10

Leu His Glu Thr Gly Gly Ala Met Val Tyr
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4  
seq SLLLVQLLTPCSA/QF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
 -25 -20 -15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
 -10 -5 1

Val Leu Xaa Xaa Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala
 5 10 15

Asp Leu
 20

```

## (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -32..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 12.6  
seq LLALLTVSTPSWC/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe Leu  
-30 -25 -20

Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser Trp Cys  
-15 -10 -5

Gln Ser Thr Glu Ala Ser Pro Lys Arg  
1 5

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.8  
seq SLLLLLLXCVHWS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Glu Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Leu Leu  
-25 -20 -15

Leu Leu Leu Leu Xaa Cys Val His Trp Ser Gln Pro Ser Leu Leu Ser  
-10 -5 1 5

Trp

(2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20 -15 -10 -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
 1 5 10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
 15 20 25

Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
 30 35 40

Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
 45 50 55 60

Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
 65 70 75

Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
 80 85 90

Thr Thr Asp Lys
 95

```

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -46..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.3  
 seq LVLLLVLTLCSL/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala  
 -45 -40 -35

Val Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly  
 -30 -25 -20 -15

Ala Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro  
 -10 -5 1

Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser  
 5 10 15

Arg Gln Lys Ala Leu Ser Pro Lys  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 345:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -16..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.1  
 seq LLLQLAVLGAALA/AA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Ala Pro Leu Leu Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala  
 -15 -10 -5

Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr  
 1 5 10 15

Lys Met Pro Ala Leu His Arg His Glu Glu Glu Lys Phe Phe Leu Asn  
 20 25 30

Ala Lys Gly Gln Lys Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr  
 35 40 45

Lys Gln Leu Ser Val Val Val Pro Ser Tyr Asn Glu Glu Lys Arg Leu  
 50 55 60  
 Pro Val Met Met Asp Glu Ala Leu Ser Tyr Leu Glu Lys Arg Gln Lys  
 65 70 75 80  
 Arg Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser  
 85 90 95  
 Lys Asp Gln Thr Ser Lys  
 100

## (2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.8  
seq SALLVGFLSVIFA/LV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Xaa Leu Leu Gly Ser Ala  
 -25 -20 -15  
 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu  
 -10 -5 1 5  
 His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn  
 10 15 20  
 Trp Xaa Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile  
 25 30 35  
 Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu  
 40 45 50  
 Leu Met Lys Ser Ile His Ala Xaa Leu Asn Ala Val Ala Ala Ile Leu  
 55 60 65  
 Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn  
 70 75 80 85  
 Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala  
 90 95 100

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq LALSLLILVLAFG/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
 -15 -10 -5

Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
 1 5 10 15

Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
 20 25 30

Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
 35 40 45

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
 50 55 60

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
 65 70 75

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
 80 85 90 95

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
 100 105 110

Gln

```

## (2) INFORMATION FOR SEQ ID NO: 348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.4  
seq AMWLLCVALAVLA/WG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp  
-15 -10 -5 1  
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu  
5 10 15  
Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala  
20 25 30  
His Pro Asp Asp Glu Ala Met Trp  
35 40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq LVFTVSLFAWICC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr  
-35 -30 -25  
Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu  
-20 -15 -10  
Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr  
-5 1 5 10

Pro Pro Tyr Lys Phe Val His Val Leu Xaa Gly Val Asp Ile Tyr Pro  
                   15                  20                  25

Glu Asn Leu Asn Ser Lys Lys Lys  
                   30

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
                                   seq GWLVLCVLAISLA/SM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser  
                   -15                  -10                  -5

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys  
                   1                  5                  10

Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys  
                   15                  20                  25                  30

Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln  
                   35                  40                  45

Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly  
                   50                  55                  60

Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile  
                   65                  70                  75

Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln  
                   80                  85                  90

Pro Arg Pro Ala Phe Ser Ala Ile Arg  
                   95                  100

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq VLLTLLLI AFIFL/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

```
Met Thr Ala Trp Glu Ala Met Ala Pro His Val Asn Pro Thr Leu Lys
 -60 -55 -50

Asp Lys Ala Leu Ser Pro Gln Gln Xaa Xaa Xaa Thr Ser Pro Ala Pro
 -45 -40 -35

Cys Xaa Ser Asn His His Asn Lys Lys His Leu Ile Leu Ala Phe Cys
 -30 -25 -20

Ala Gly Val Leu Leu Thr Leu Leu Leu Ile Ala Phe Ile Phe Leu Ile
 -15 -10 -5 1

Ile Lys Ser Tyr Arg Lys Tyr His Ser Lys Pro Gln Ala Pro Gly
 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLCECLLLXAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:



Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Xaa Ala Gly  
                   -15                  -10                  -5

Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr  
                   1                                  5                                  10

Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala Lys Tyr Gly Ile  
   15                                  20                                  25                                  30

Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys Ala Xaa Glu Ile  
                                   35                                  40                                  45

Ser Glu

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq LVXSLPVHCLTFA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Met Gly His Ala Met Gly Leu Val Xaa Ser Leu Pro Val His Cys Leu  
                   -15                  -10                  -5

Thr Phe Ala Ser Ser Ala Pro Ser Ser Pro Gln Pro Thr Arg Met Trp  
                   1                                  5                                  10

Phe Xaa Ala Gln Ala His Xaa Pro Pro Leu Ile Leu Gly Pro  
   15                                  20                                  25

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq CFSLVLLTTSIWT/TR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Thr Ser Ile Trp Thr  
-15 -10 -5  
Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
1 5 10 15  
Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
20 25 30  
Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
35 40 45  
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
50 55 60  
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
65 70 75 80  
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
85 90 95  
Val Leu Ile Trp  
100

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -59..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq VLAQLAFLSQISQ/CI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser  
                               -55                              -50                              -45

Ile His Arg Gln His Ser Lys Asp Leu Gln Asp Ile Val Ala Thr Leu  
                               -40                              -35                              -30

Gly Pro Arg Ser Ala Thr His Pro His Gln Pro Ala Ile Gln Val Leu  
                               -25                              -20                              -15

Ala Gln Leu Ala Phe Leu Ser Gln Ile Ser Gln Cys Ile Ile Ser Gln  
                               -10                              -5                              1                              5

Arg

## (2) INFORMATION FOR SEQ ID NO: 356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq IVSLLGFVATVTL/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile  
                               -25                              -20                              -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe  
                               -10                              -5                              1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys  
   5                              10                              15                              20

Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly Val Ile Ser Gly Ala  
                               25                              30                              35

Val Phe Leu Ile Ile Leu Phe Cys  
                               40

## (2) INFORMATION FOR SEQ ID NO: 357:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

```
Met Phe Lys Val Ile Gln Arg Ser Val Gly Pro Ala Ser Leu Ser Leu
 -20 -15 -10

Leu Thr Phe Lys Val Tyr Ala Ala Pro Lys Lys Asp Ser Pro Pro Lys
 -5 1 5

Asn Ser Val Lys Val Asp Glu Leu Ser Leu Tyr Ser Val Pro Glu Gly
 10 15 20 25

Gln Ser Lys Tyr Val Glu Glu Ala Arg Ser Gln Leu Glu Glu Ser Ile
 30 35 40

Ser Gln Leu Arg His Tyr Cys Glu Pro Tyr Thr Thr Trp Cys Gln Glu
 45 50 55

Thr Tyr
```

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -136..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu Ser Gly Arg Thr Lys  
 -135 -130 -125

Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser Thr Ser His Gly Phe  
 -120 -115 -110 -105

Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln Phe Pro Gly Gly Ser  
 -100 -95 -90

Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly Ile Leu Thr Leu Asn  
 -85 -80 -75

Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val Met Met Leu Gln Leu  
 -70 -65 -60

Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr Glu Gly Lys Gly Leu  
 -55 -50 -45

Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser Gly Ser Asp Leu Asn  
 -40 -35 -30 -25

Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro Leu Ile Ser Val Ala  
 -20 -15 -10

Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala Ala  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq PLLKILHAAGAQQ/EM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser Asp Ser Ala  
 -40 -35 -30

Cys Arg Ile Ser Pro Gly Gln Ile Asn Xaa Val Arg Pro Lys Leu Pro  
 -25 -20 -15

Leu Leu Lys Ile Leu His Ala Ala Gly Ala Gln Gly Glu Met Phe Thr

-10

-5

1

Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met Val Lys Gln  
 5 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq AFAWLGVVPLTAC/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu Gly  
 -110 -105 -100

Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser Ile  
 -95 -90 -85

Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser Arg  
 -80 -75 -70 -65

Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro Ile  
 -60 -55 -50

Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe Ala  
 -45 -40 -35

Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His Tyr  
 -30 -25 -20

Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala Cys  
 -15 -10 -5

Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu Thr  
 1 5 10 15

Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys Leu  
 20 25 30

Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile  
 35 40 45

## (2) INFORMATION FOR SEQ ID NO: 361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq MLIMLGIFNVHS/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu  
-10 -5 1  
Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Xaa Gly Pro Gln  
5 10 15  
Asn Ile Tyr Asn Leu Tyr Glu His Gly  
20 25

## (2) INFORMATION FOR SEQ ID NO: 362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq AAVAVGMLXASYA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Gly Leu Trp Arg Pro Gly Trp Arg Cys Val Pro Phe Cys Gly  
-110 -105 -100

Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu Arg Val  
     -95                    -90                    -85  
 Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala Glu Arg  
     -80                    -75                    -70                    -65  
 Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg Ala Arg  
                     -60                    -55                    -50  
 His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn Pro Phe  
                     -45                    -40                    -35  
 Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr Thr Leu  
             -30                    -25                    -20  
 Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser Tyr Ala  
     -15                    -10                    -5  
 Ala Val  
 1

## (2) INFORMATION FOR SEQ ID NO: 363:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SDPLCVLFLNTSG/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val Ser Cys Ala  
                     -35                    -30                    -25  
 Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro Leu Cys Val  
                     -20                    -15                    -10  
 Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val Glu Arg Thr  
             -5                    1                    5  
 Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys Thr Phe Ile  
     10                    15                    20                    25  
 Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe Gly Val Tyr  
             30                    35                    40



Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp Phe Leu Gly  
 45 50 55

## (2) INFORMATION FOR SEQ ID NO: 364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq AVLDCAFYDPHTA/WS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly  
 -70 -65 -60 -55

Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val  
 -50 -45 -40

Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser  
 -35 -30 -25

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe  
 -20 -15 -10

Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Xaa Xaa Lys  
 -5 1 5 10

Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp  
 15 20 25

Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Ser  
 30 35

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq AHLWCWCGSHCCST/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

```

Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys
-25 -20 -15 -10
Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
 -5 1 5
Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp
 10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -13..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq MLAVSLTVXLLGA/MM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```

Met Leu Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu
 -10 -5 1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
 20 25 30 35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50

```

Gly Asp Val Met Phe Thr Gly Ser Trp  
55 -60

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -76..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq MLELDLLVFHLWG/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Ser Ser Thr Leu Ala Lys Ile Ala Glu Ile Glu Ala Glu Met Ala  
-75 -70 -65

Arg Thr Gln Lys Asn Lys Ala Thr Ala His His Leu Gly Leu Leu Lys  
-60 -55 -50 -45

Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu Ile Thr Pro Lys Gly Gly  
-40 -35 -30

Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp Trp Pro Arg Gln Val Met  
-25 -20 -15

Leu Glu Leu Asp Leu Leu Val Phe His Leu Trp Gly Ser Gln His Cys  
-10 -5 1

Leu Val Thr Trp Gln Gly  
5 10

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.9  
seq LVLALLLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45 -40 -35 -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
 -25 -20 -15

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val
 -10 -5 1

Ser Arg Thr Asp Ser Pro Ser Pro Leu
5 10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.9  
seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
-25 -20 -15 -10

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
 -5 1 5

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
10 15 20

Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6  
seq ILLCLLLALFASG/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```

Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
 -85 -80 -75

Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
 -70 -65 -60

Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
 -55 -50 -45

Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
 -40 -35 -30 -25

Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
 -20 -15 -10

Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
 -5 1 5

Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
 10 15 20

Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
 25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6  
seq VFCLLAVAPGAHS/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly  
-15 -10 -5

Ala His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys  
1 5 10

Pro Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe  
15 20 25

Thr Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu  
30 35 40 45

Glu Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala  
50 55 60

Gln Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn  
65 70 75

Ile Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val  
80 85 90

Tyr Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu  
95 100 105

Asp Ala Leu Asp Leu Trp  
110 115

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -113...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6

seq ILLCLLLALFASG/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

```

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Ser Pro Phe Leu Ala Arg
 -110 -105 -100

Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
 -95 -90 -85

Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
 -80 -75 -70

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
 -65 -60 -55 -50

Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
 -45 -40 -35

Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys
 -30 -25 -20

Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser
 -15 -10 -5

Gly Leu Ile His Arg Val Cys Val Thr Thr Cys Phe Ile Phe Ser Met
 1 5 10 15

Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4  
seq LMSLLLVLPVVEA/VE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

```

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 -20 -15 -10

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

```

-5                                  1                                  5  
Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Val Pro Ala Trp  
      10                                          15                                  20  
  
Gly Tyr Met His Gly  
      25

## (2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -20..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 11.2  
                                  seq ILVVLMLPLAQA/LD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro  
-20                                  -15                                  -10                                  -5  
  
Leu Ala Gln Ala Leu Asp Cys His Val Cys Xaa Tyr Asn Gly Asp Asn  
                                  1                                          5                                          10  
  
Cys

## (2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -16..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 11



seq LLALSLLVLWTSP/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
-15 -10 -5

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
 1 5 10 15

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
 20 25 30

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
 35 40 45

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
 50 55 60

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Xaa Arg
 65 70 75 80

Ser Ser Xaa Pro Met Xaa Val Xaa Arg Glu Pro Glu Ser Glu Ser Ser
 85 90 95

Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa Arg
100 105

```

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq RLLLLPLLLAVSG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Pro Leu Leu
-20 -15 -10

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
-5 1 5 10

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met

```

```

 15 20 25
Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
 30 35 40
Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Xaa Thr Arg
 45 50 55
Lys Gln Arg Ile Thr Glu Thr Gly Ser Pro Tyr Gln Glu Leu Gln Gly
 60 65 70 75
Gln Arg Ser Asp Val Tyr Ser
 80

```

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq LCRALCLFPRVFA/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 -20 -15 -10
Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 -5 1 5
Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro
 10 15 20
Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys
 25 30 35 40
Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Leu Ile Ser Val Arg Arg
 45 50 55
Gln Leu

```

## (2) INFORMATION FOR SEQ ID NO: 378:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LMCLSLCTAFALS/KP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe  
                  -15                  -10                  -5

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro  
                  1                                  5                                  10

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Xaa Tyr Asp  
          15                                  20                                  25

His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa Phe Asp Gln Leu  
          30                                  35                                  40                                  45

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile  
                  50                                  55                                  60

Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys  
                  65                                  70                                  75

## (2) INFORMATION FOR SEQ ID NO: 379:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LLFLSQFCILSGG/ES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg  
 -30                               -25                               -20                               -15

Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser  
                               -10                               -5                               1

Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys  
                               5                               10                               15

Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser Thr Thr Asn Phe Ser Cys  
                               20                               25                               30

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Xaa Val Lys Pro Ser Val  
                               35                               40                               45                               50

Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Xaa Phe Ile Ile Asn  
                               55                               60                               65

Met Thr Cys

## (2) INFORMATION FOR SEQ ID NO: 380:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
 -20                               -15                               -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala  
 -5                               1                               5                               10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser  
                               15                               20                               25

Gly Lys Asn Tyr Phe Ser Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr  
                               30                               35                               40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile

45

50

55

Xaa Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
60 65 70 75

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
80 85 90

Gly Leu Ser Gly Lys Trp  
95

## (2) INFORMATION FOR SEQ ID NO: 381:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq LLWLALACSPVHT/XL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
-15 -10 -5

Val His Thr Xaa Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Arg  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.3  
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
-15 -10 -5

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
 1 5 10 15

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ile Met Met Xaa Leu Gly Xaa
 20 25 30

Xaa Phe Thr Ile Asp Tyr Xaa Ile Phe Glu Ser Glu
 35 40

```

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/S?

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
-20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
-5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
 45 50 55

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
 60 65 70 75

```

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu  
80 85

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.2  
seq LLXLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Arg Thr Leu Phe Asn Leu Leu Xaa Leu Ala Leu Ala Cys Ser Pro  
-15 -10 -5  
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
1 5 10  
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
15 20 25  
Gly Leu Val Val Thr Asp Gly  
30 35

## (2) INFORMATION FOR SEQ ID NO: 385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9

seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```

Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
-40 -35 -30 -25

Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
 -20 -15 -10

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa
 -5 1 5

Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro
10 15 20

Cys Thr Gly Gly Met Glu
25 30

```

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

```

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
 -25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
 -10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
20 25 30 35

Val Lys Pro His Met
 40

```



## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq SAVLSGFVLGALA/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu Gly
 -15 -10 -5

Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu Gly Phe
 1 5 10

Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile Thr Asp Ser
 15 20 25

Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp Ile Gln Lys Tyr
 30 35 40 45

Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn Ser Ser Gly Glu Val
 50 55 60

Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser Asn Val Lys Lys Asn Val
 65 70 75

Val Gly Trp Tyr Lys Phe Arg Arg His Ser Asp Gln Ile Met Thr Phe
 80 85 90

Arg Glu Arg Leu Leu His Lys Asn Leu Gln Glu His Phe Ser Asn Gln
 95 100 105

Asp Leu Val Phe Leu Leu Leu Thr Pro
 110 115

```

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -32..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
-30 -25 -20  
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
-15 -10 -5  
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
1 5 10 15  
Asp Pro Glu Arg  
20

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -136..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.7  
seq AVALSLFLGWLGA/DR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser Ala Pro Glu Ala Val Thr  
-135 -130 -125  
Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro  
-120 -115 -110 -105  
Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys  
-100 -95 -90

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn  
                   -85                                  -80                                  -75  
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val  
                   -70                                  -65                                  -60  
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn  
                   -55                                  -50                                  -45  
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser  
                   -40                                  -35                                  -30                                  -25  
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser  
                                   -20                                  -15                                  -10  
 Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg Phe  
                                   -5                                                          1

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq LLWLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
                   -15                                  -10                                  -5  
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Thr Ser Gly  
                   1                                  5                                  10

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq ASLFLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu  
-40 -35 -30  
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu  
-25 -20 -15  
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala  
-10 -5 1 5  
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr  
10 15 20  
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe  
25 30 35  
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser  
40 45

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.5  
seq LVLGLVLPILWA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Val Ala Pro Gly Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu  
-15 -10 -5  
Trp Ala Asp Arg Ser Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile  
1 5 10

Asn Asn Asp Met Val Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp  
 15 20 25 30  
 Gly Phe Gly Thr Pro Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly  
 35 40 45  
 Gln Glu Thr Ile Met Lys Lys Val Thr Ser Val Lys Ala His Ser Asp  
 50 55 60  
 Thr Trp Met Val Val Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu  
 65 70 75  
 Val Met Ala Gln Gln Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val  
 80 85 90  
 His Asp Val Leu Phe Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn  
 95 100 105 110  
 Met Gln Met Thr Ala Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu  
 115 120 125  
 Leu

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq LLTIVGLILPTRG/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile  
 -20 -15 -10  
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser  
 -5 1 5 10  
 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp  
 15 20 25  
 Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Trp Pro  
 30 35 40

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly  
 45 50 55  
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr Pro Arg  
 60 65 70

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LALSSLLSLLLFA/GM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe Leu Ala Arg  
 -45 -40 -35  
 Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly  
 -30 -25 -20  
 Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly  
 -15 -10 -5 1  
 Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile  
 5 10 15  
 Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala  
 20 25 30  
 Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys  
 35 40 45  
 Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser  
 50 55 60 65  
 Gly Pro

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.3  
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```
Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln
-35 -30 -25 -20

Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg
 -15 -10 -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
 1 5 10

Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly
 15 20 25

Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe
 30 35 40 45

Ile Glu Cys Glu Asp Arg
 50
```

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -53..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.1  
seq IYALFLLVGVCA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

```

Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys
 -50 -45 -40

Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly
 -35 -30 -25

Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val
 -20 -15 -10

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln
 -5 1 5 10

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro
 15 20 25

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly
 30 35 40

Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys
 45 50 55

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe
 60 65 70

```

## (2) INFORMATION FOR SEQ ID NO: 397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -57..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq IVRLVAFCPFASS/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

```

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu
 -55 -50 -45

Leu Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val
 -40 -35 -30

Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu
 -25 -20 -15 -10

Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala
 -5 1 5

```



Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu  
           10                                  15                                  20  
 Glu Thr His Leu Pro Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly  
           25                                  30                                  35  
 Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys  
           40                                  45                                  50                                  55  
 Gln Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Xaa Val Arg Leu His  
                                   60                                  65                                  70  
 Phe His Asn Leu Val Lys Gly Ser Asp Arg Cys Xaa Gln Leu Val Lys  
                                   75                                  80                                  85  
 His Ser Trp Gly Trp Asp Thr Ala Ile Pro Met  
           90                                  95

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser  
           -45                                  -40                                  -35  
 Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser  
           -30                                  -25                                  -20  
 Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser  
           -15                                  -10                                  -5                                  1  
 Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ile Gly  
                                   5                                  10                                  15

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Leu Leu Val Gly  
-25 -20 -15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly  
-10 -5 1 5

Gln Glu Pro Leu His Asn Glu Glu Pro Gly  
10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

-15

-10

-5

Leu Pro Thr Gln Xaa Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
 1 5 10 15  
 Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
 20 25 30  
 Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
 35 40 45  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
 50 55 60  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
 65 70 75 80  
 Pro Pro Leu

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPPLCHG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa Xaa Ala  
 -65 -60 -55  
 Val Thr Ala Xaa Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val  
 -50 -45 -40  
 Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu  
 -35 -30 -25  
 Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro  
 -20 -15 -10  
 Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys  
 -5 1 5 10  
 Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile  
 15 20 25

Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Ala  
 30 35 40  
 Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg  
 45 50 55  
 Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe  
 60 65 70 75  
 Leu Met Thr Cys

## (2) INFORMATION FOR SEQ ID NO: 402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq LLMLLLFLSELQY/YL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr  
 -45 -40 -35  
 Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile  
 -30 -25 -20  
 Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr  
 -15 -10 -5  
 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg  
 1 5 10 15  
 Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro  
 20 25 30  
 Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln  
 35 40 45  
 Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly  
 50 55 60  
 Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu  
 65 70 75 80

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro  
85 90

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPLCHG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
-15 -10 -5

Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe Asp Trp Arg  
1 5 10 15

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
20 25 30

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
35 40 45

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
50 55 60

Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
65 70 75 80

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe Asn Asp Lys  
85 90 95

## (2) INFORMATION FOR SEQ ID NO: 404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala  
                  -15                  -10                  -5  
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val  
                  1                          5                          10  
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met  
          15                          20                          25  
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu  
          30                          35                          40                          45  
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala  
                  50                          55                          60  
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg  
                  65                          70                          75  
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile  
          80                          85                          90  
Ala Cys Lys Leu Cys  
          95

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 131 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4

seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
 -15 -10 -5

Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
 1 5 10

Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met
 15 20 25

Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu
 30 35 40 45

Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Xaa
 50 55 60

Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
 65 70 75

Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile
 80 85 90

Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile
 95 100 105

Glu Ala Glu
110

```

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4

seq ILPLLFGCLGVFG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 -20 -15 -10

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5 1 5 10
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15 20 25
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30 35 40
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45 50 55
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60 65 70 75
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80 85 90
Glu Ile Cys Ser
95

```

## (2) INFORMATION FOR SEQ ID NO: 407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LLLVTWVETPVTT/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu
-25 -20 -15
Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
-10 -5 1
Ser Leu Asp Thr Glu Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
5 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

```
Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr
-20 -15 -10 -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp
 1 5 10

Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe
 15 20 25

Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Phe Arg
 30 35 40
```

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq ALSLLLVSGLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```
Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
 -20 -15 -10

Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| -5  |     |     |     |     | 1   |     |     |     |     | 5   |     |     |     |     |     |
| Arg | Ile | Val | Thr | Ser | Glu | Glu | Val | Ile | Ile | Arg | Asp | Ser | Pro | Val | Leu |
| 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |
| Pro | Val | Thr | Leu | Gln | Cys | Asn | Leu | Thr | Ser | Ser | Ser | His | Thr | Leu | Thr |
|     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |
| Tyr | Ser | Tyr | Trp | Thr | Lys | Asn | Gly | Val | Glu | Leu | Ser | Ala | Thr | Arg | Lys |
|     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |
| Asn | Ala | Ser | Asn | Met | Glu | Tyr | Arg | Ile | Asn | Lys | Pro | Arg | Ala | Glu | Asp |
|     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |
| Ser | Gly | Glu | Tyr | His | Cys | Val | Tyr | His | Phe | Val | Ser | Ala | Pro | Lys | Ala |
|     | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |
| Asn | Ala | Thr | Ile | Glu | Val | Lys | Ala | Ala | Pro | Asp | Ile | Thr | Gly | His | Lys |
| 90  |     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |     | 105 |
| Arg | Ser | Xaa | Asn | Lys | Asn | Glu | Gly | Gln | Asp |     |     |     |     |     |     |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

(1X) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.2
                        seq IMLLSLAAFSVIS/VV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly
-35 -30 -25

Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe
-20 -15 -10 -5

Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val
1 5 10

Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys
15 20 25

Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr

30

35

40

Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His
 45 50 55 60

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTL LLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Xaa Gly Ser Val Glu Cys Thr Xaa Gly Trp Gly His Cys Ala Pro
 -30 -25 -20

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
 20 25 30

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45

Val Met Val Ala Thr Asn Thr Pro Pro Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
-25 -20 -15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
-10 -5 1
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
5 10 15
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
20 25 30 35
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa Gly Ala Lys Xaa
40 45 50
Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile
55 60 65
Phe

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly His Cys Ala Pro
-30 -25 -20
Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

```

Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65                      -60                      -55                      -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
                      -45                      -40                      -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
                      -30                      -25                      -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
                      -15                      -10                      -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
      1                      5                      10                      15

Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
                      20                      25                      30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
      35                      40                      45

Val Trp Lys Thr
      50

```

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -154..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

```

Met Ala Leu Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
      -150                      -145                      -140
Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Xaa Asp Gly Tyr
      -135                      -130                      -125
Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
      -120                      -115                      -110
Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
      -105                      -100                      -95
Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
      -90                      -85                      -80                      -75
Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
      -70                      -65                      -60
Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
      -55                      -50                      -45
Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
      -40                      -35                      -30
Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
      -25                      -20                      -15
Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
      -10                      -5                      1                      5
Lys Ala Thr

```

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -70..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LAFSLPALPLAEL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

```

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
-70                               -65                               -60                               -55
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
                               -50                               -45                               -40
Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
                               -35                               -30                               -25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
                               -20                               -15                               -10
Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
                               -5                               1                               5                               10
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
                               15                               20                               25
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
                               30                               35                               40
Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser
                               45                               50                               55

```

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.6
 seq KMVHLLVLSGAWG/MQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

```

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
                               -20                               -15                               -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val

```


[illegible]

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -81..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq LLASGTTLFCTS/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

```

Met Ala Gly Pro Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly
  -60                               -70
Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Xaa Phe
-65                               -55                               -50
Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His
      -45                               -40                               -35
Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro
      -30                               -25                               -20
Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr
      -15                               -10                               -5
Ser Phe Tyr Tyr Gln Ala Gln
    1                               5

```

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq LLTLLPPPLYT/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
-20 -15 -10
Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
-5 1 5 10
Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
15 20 25

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq ILFLLPSICSSNS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys
-20 -15 -10 -5
Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala Leu Ala Ala
-15 -10 -5 1
Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp Pro Trp Lys
 5 10 15
Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Gln Gln Val Ser Asn
 20 25 30
Leu Ile His Tyr Leu Gly Leu Ser His His Leu Leu Ala Leu Asn Phe
 35 40 45
Ile Ile Val Ser Phe Gly Lys Lys Ser Ala Trp Ser Ser Ala Gln Val
 50 55 60 65
Lys Val Thr Asp Thr Asp Phe Asp Gly Val Glu Val Arg Val Phe Glu
 70 75 80
Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys Arg Ser Val Val Tyr Ile
 85 90 95
His Gly Xaa Gly Trp
 100

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Met
40 45

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -69..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq ILLIVLFLDAVRE/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Thr Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile
-65 -60 -55
Gly Leu Ile Leu Ile Phe Cys Leu Pro Phe Ile Pro Pro Gln Arg Trp
-50 -45 -40
Gln Lys Ile Phe Ser Phe Asn Val Trp Gly Lys Ile Ala Thr Phe Trp

-35 -30 -25
 Asn Lys Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu
 -20 -15 -10
 Asp Ala Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu
 -5 1 5 10
 Lys Ser Ser Thr Ser Arg Pro Arg
 15

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq FLDFCVYIPLSWG/FC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
 -85 -80 -75 -70
 Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
 -65 -60 -55
 Glu Val Ser Gly Gly Pro Gly Gly Arg Arg Pro Phe Arg Pro Leu Ala
 -50 -45 -40
 Thr Glu Thr Phe Ser Leu Ala Val Gly Thr Phe Cys Ser Arg Glu Pro
 -35 -30 -25
 Val Gln Ser Asn Asn Leu His Leu Phe Leu Asp Phe Cys Val Tyr Ile
 -20 -15 -10
 Pro Leu Ser Trp Gly Phe Cys Pro Leu Gln Pro Ile Leu Ala
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq AILGSTWVALTTG/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
 -20 -15 -10
Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
 -5 1 5
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
 10 15 20
Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe
 25 30 35 40
His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu
 45 50 55
Ala Arg Ala Asp Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa
 60 65 70
Pro Phe Leu Cys Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro
 75 80 85
Gly

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.2
seq FLVSNMLLAAYG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

```

Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
-20                      -15                      -10

Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
-5                      1                      5                      10

Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
15                      20                      25

Trp Leu Asp Ala Gln Ser Gly
30

```

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq SVLVLLLLAVLYE/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe His
-40                      -35                      -30

Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu Val
-25                      -20                      -15                      -10

Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys Ala
-5                      1                      5

Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser Gln
10                      15                      20

Gln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser Phe
25                      30                      35

Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly Gln
40                      45                      50                      55

```


Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met Leu
60 65 70
Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val
75 80 85

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VVXXSVLXTTCXS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala
-75 -70 -65 -60
Gln Ala Gln Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg
-55 -50 -45
Leu Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile
-40 -35 -30
Asp Ala Gly Xaa Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val
-25 -20 -15
Xaa Xaa Ser Val Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq LLAALMLVAMLQL/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```

Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr Gln Leu Leu Leu
  -25                      -20                      -15

Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu Tyr Leu Ser Leu
  -10                      -5                      1                      5

Leu Ser Gly Leu His Gly Pro
                      10

```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```

Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val
      -15                      -10                      -5

Cys Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro
      1                      5                      10

Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr Ala Pro Met
  15                      20                      25

Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro Glu
  30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```
Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe
   -20                      -15                      -10

Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
   -5                      1                      5                      10

Leu Gln Cys Ser Val Gly Ile
                   15
```

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LMAFLLSFYLIPT/NE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```
Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys
   -50                      -45                      -40

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
   -35                      -30                      -25
```

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
-20 -15 -10 -5
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
1 5 10
Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
15 20 25
Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile
30 35 40

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LEMLTAFASHIRA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr Ala Phe Ala
-20 -15 -10
Ser His Ile Arg Ala Arg Asp Ala Ser Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Val His Lys Pro Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile
 -20 -15 -10
His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr
 -5 1 5
Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
 10 15 20
Thr Thr
 25

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
 -25 -20 -15
Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
 -10 -5 1
Tyr Trp Pro Thr
 5

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val
-20 -15 -10
Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr
-5 1 5 10
Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile
15 20 25
Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu
30 35 40
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln
45 50 55
Met Arg Asn Ser Gln Ala His Arg
60 65

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -87...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9
seq SNILLASVGSVLG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val

-85 -80 -75
 Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
 -70 -65 -60
 Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile
 -55 -50 -45 -40
 Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
 -35 -30 -25
 Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
 -20 -15 -10
 Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Xaa
 -5 1 5
 Ser Leu Pro Ala Glu Pro Xaa Xaa Xaa Glu Asp Glu Ala Arg Glu Asn
 10 15 20 25
 Val Pro Pro

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq VTIIILLSCXFWA/VK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Val Thr Ile Ile Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys
 -10 -5 1
 Asn Val Thr Xaa Arg Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -87..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.8
seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Xaa Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
  -85                               -80                               -75

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
  -70                               -65                               -60

Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile
  -55                               -50                               -45                               -40

Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
  -35                               -30                               -25

Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
  -20                               -15                               -10

Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser
  -5                               1                               5

Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn
  10                               15                               20                               25

Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His
  30                               35                               40

Glu Arg

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -89..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq DLSLLSLPPGTSP/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
      -85                      -80                      -75

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Xaa Xaa Gly Arg Asn
      -70                      -65                      -60

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu
      -55                      -50                      -45

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
      -40                      -35                      -30

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu
      -25                      -20                      -15                      -10

Leu Ser Leu Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu
      -5                      1                      5

Ala Pro Ile Pro Pro Thr Xaa Leu Ala Xaa Ala Xaa Cys Trp Ala Pro
      10                      15                      20

Ser Val Arg Trp Thr Cys
      25
  
```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LLLPRVLLTMASG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

```

Met Pro Xaa Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
      -20                      -15                      -10

Val Leu Leu Thr Met Ala Ser Gly Ser Leu Arg Xaa Ser Xaa Arg Arg
      -5                      1                      5
  
```

Pro Arg Ile Pro Xaa Leu Ala Thr Phe Arg Xaa Arg Ser Leu
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq IFSELDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
 -35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
 -15 -10 -5

Cys Arg Cys Ala Gln Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp
 1 5 10

Gly Ser Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val
 15 20 25

Glu Gly Arg Val Val Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu
 30 35 40 45

Arg Lys Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu
 50 55 60

Xaa Thr Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn
 65 70 75

Gly Cys Thr Lys Ile Thr Xaa Ser Thr Cys
 80 85

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
-35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
-15 -10 -5

Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp
1 5 10

Gly Ser Asn Trp Gln Gly
15

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -112..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq SSCILPWLSKTNS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu Pro Ser Asp Pro Glu
-110 -105 -100

Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala Arg Ser Leu Phe
-95 -90 -85

```

Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val Asp Trp Asp His
-80                -75                -70                -65

His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu Asn Leu Pro Arg
                -60                -55                -50

Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys Pro Val Cys Leu
                -45                -40                -35

Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met Pro Cys His His
                -30                -25                -20

Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser Lys Thr Asn Ser
                -15                -10                -5

Cys Pro Leu Cys Arg Tyr Glu Leu Pro Thr Asp Asp Asp Thr Tyr Glu
  1          5          10          15

Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln Gln His Arg Pro
                20                25                30

```

Xaa

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15                -10                -5                1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
          5          10          15

Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln Pro Ser Pro
          20          25          30

Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu Gln Pro Arg
          35          40          45

Pro Gly

```

50

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: S adrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LRRLLGCLTLTLS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Leu Gly Ile Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu
-70 -65 -60

Gly Leu Glu Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly
-55 -50 -45

Ser Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn
-40 -35 -30

Glu Ala Arg Gly Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu
-25 -20 -15 -10

Leu Gly Cys Leu Thr Leu Thr Leu Ser Gly Arg Ile
-5 1

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq ALKLASWTSMALA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
  -15                      -10                      -5
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
   1                      5                      10                      15
Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
                20                      25                      30
Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
                35                      40                      45
Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
                50                      55                      60
Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
   65                      70

```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq AALPAWLSLQSR/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

```

Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser Arg Ala
  -15                      -10                      -5
Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr Pro Val
   1                      5                      10                      15
Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro
                20                      25                      30
Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Asp Gln
   35                      40                      45

```

```

Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro Ser Ala
  50              55              60

Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro
  65              70              75              80

Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn Phe Leu
              85              90              95

His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu Lys Asp
      100              105              110

Phe Cys Thr Glu
      115

```

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CMLTLXXLSFILA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

```

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65              -60              -55              -50

Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
      -45              -40              -35

Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
      -30              -25              -20

Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
      -15              -10              -5

Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
  1              5              10              15

Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
      20              25              30

Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
      35              40              45

```

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
-45 -40 -35

Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val Ala Ala Thr
-30 -25 -20

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
-15 -10 -5

Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
1 5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LXGFLFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val Ile Val Leu
 -15 -10 -5
 Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg Trp Gly Cys
 1 5 10
 Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr Pro Asp Asn
 15 20 25 30
 Phe Cys Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq VVFM TVAASGASS/FA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu
 -25 -20 -15
 Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe Ala Val
 -10 -5 1
 Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
 5 10 15
 Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr
 20 25 30 35
 Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg
 40 45 50
 Val Thr

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Glu Leu Ala His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln
-15 -10 -5 1
Ile Thr Glu Ala Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe
 5 10 15
Leu Asp Lys Val Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys
 20 25 30
Gln Lys Lys Leu Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro
 35 40 45
Gly Pro Thr Gly
50

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAVLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu
 -25 -20 -15

```
Met Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr  
-30 -25 -20
```

Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
-15 -10 -5 1

Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
5 10 15

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
20 25 30

Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
35 40 45

Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa Ser Gly Asn
50 55 60 65

Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
70 75 80

Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa Xaa Val Ser
85 90 95
Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
100 105 110
Phe Gly Phe Val
115

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
5 10 15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
 -10 -5 1

Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg Asp Leu Gln Gln
 5 10 15

Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser
 20 25 30 35

Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile
 40 45 50

Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro
 55 60 65

Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
 70 75 80

Glu Gln
 85

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
 seq MMVLSLGIXLASA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55

Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40

Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
 -35 -30 -25

Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10

Xaa Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
 15 20 25
 Ile Ser Gly Ser Leu Ser Ile
 30

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Gly Val Gly Lys Xaa Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85
 Ala Val Xaa Leu Ile Thr Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys
 90 95 100
 Thr Phe Val Thr Trp Phe Leu
 105 110

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
-25                -20                -15                -10

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
          -5                1                5

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
    10                15                20

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
    25                30                35

Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
    40                45                50                55

Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
          60                65                70

Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
          75                80                85

Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
    90                95                100

Thr Phe Val His Val Val Pro
    105                110

```

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AIALATVLFLLGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
-55 -50 -45
Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
-40 -35 -30
Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
-25 -20 -15 -10
Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
-5 1 5
Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
10 15 20
Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
25 30 35

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp

-15 -10 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
 5 10 15

Gln His Pro Thr Xaa Gln
 20

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15 -10 -5 1
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
5 10 15
Gln His Pro Thr Gln Cys Ser Thr His Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(v) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -68..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

```

Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
      -65                      -60                      -55
Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
      -50                      -45                      -40
Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
      -35                      -30                      -25
Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
      -20                      -15                      -10                      -5
His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
              1              5              10
Ala

```

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -94..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VILQLQFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```

Met Phe Gly Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln
      -90                      -85                      -80
Arg Asp Ser Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly
      -75                      -70                      -65
Asp Val Val Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr
      -60                      -55                      -50
Leu Gln Gln Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly
      -45                      -40                      -35
Pro Gly Gln Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser

```

PCT/IB98/01222

-15

Leu Ser Leu Lys Leu Val His Val Ala Gly Pro Gly Pro Thr
5 10 15

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq WYSTVGLLPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys Asp His Gly Thr
-35                -30                -25                -20

Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly Leu Leu Pro Pro
                -15                -10                -5

Val Arg Ala Met Ser Gln Arg Asn Leu Asn
                1                5

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq ARALAALVPGVTQ/VD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Ala Ala Ala Leu Lys Cys Leu Leu Thr Leu Gly Arg Trp Cys Pro
-35                -30                -25

Gly Leu Gly Val Ala Pro Gln Ala Arg Ala Leu Ala Ala Leu Val Pro
-20                -15                -10                -5

Gly Val Thr Gln Val Asp Asn Lys Ser Gly Phe Leu Gln Lys Arg Pro
                1                5                10

His Arg Gln His Pro Gly Ile Leu Lys Leu Pro His Val Arg Leu Pro
                15                20                25

```

Gln Ala Leu Ala Asn Gly Ala Gln Leu Leu Leu Leu Gly Ser Ala Gly
 30 35 40

Pro Thr Met Glu Asn Gln Val Gln Thr Leu Thr Ser Tyr Leu Trp Ser
 45 50 55 60

Arg His Leu Pro Val Glu Pro Xaa Glu Leu Gln Arg Arg Ala Xaa His
 65 70 75

Leu Glu Lys Lys Phe Leu Glu Asn Pro Asp Leu Ser Gln Thr Glu Glu
 80 85 90

Lys Leu Arg Gly Ala Gly
 95

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -102..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq TVMSALSVAPSKA/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu Ile Lys Gly Ser
 -100 -95 -90

Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly
 -85 -80 -75

Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val
 -70 -65 -60 -55

Pro Pro Ala Met Xaa Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly
 -50 -45 -40

Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile
 -35 -30 -25

Arg Asp Ser Trp Xaa Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser
 -20 -15 -10

Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr
 -5 1 5 10

Val Lys Ala Leu Gly
15

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Val Asn Glu Leu Gln Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala
-15 -10 -5

Cys Ser Ser Ser Lys Gln Arg Phe
1 5

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FFESIQPFLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala Phe Phe Phe Ser Ile

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
-70 -65 -60 -55

Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
 -50 -45 -40

Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn
 -35 -30 -25

Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe
 -20 -15 -10

Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg
 -5 1 5 10

Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn
 15 20 25

Tyr Leu Tyr

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9

seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
-55                      -50                      -45

Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser
-40                      -35                      -30                      -25

Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
                      -20                      -15                      -10

Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly
                      -5                      1                      5

Pro Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro
10                      15                      20

Phe Val
25

```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Glu Glu Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys
-25                      -20                      -15

Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
-10                      -5                      1                      5

Ser Val Arg Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser
10                      15                      20

Lys His Leu Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp
25                      30                      35

```

Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys
40 45 50

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LXXVVAFVAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Val Arg Arg Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu
-15 -10 -5

Ser Gln Gln Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly
1 5 10 15

Gln Glu Arg Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly
20 25 30

Asp Cys Gln Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp
35 40 45

Gly Ser Asp Val Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys
50 55 60

Thr Lys Glu Ala Gly Asp Gly Pro Leu
65 70

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq PIVRLLSCPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn Leu Cys Ala
-35 -30 -25

Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu Leu Ser Cys
-20 -15 -10

Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln Pro Ser Gly
-5 1 5 10

Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg Arg Phe Ser
15 20 25

Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr Val Leu Ile
30 35 40

His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys Tyr Leu Ser
45 50 55

Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser Phe Gly Leu
60 65 70 75

Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly Ser Leu Gln
80 85 90

Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala Ile Pro Phe
95 100 105

Arg Ser Arg Ser Ser
110

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LVILSLKSQTLDA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
-60          -55          -50          -45

Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
          -40          -35          -30

Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
          -25          -20          -15

Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
          -10          -5          1

Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
  5          10          15          20

Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Xaa
          25          30          35

Asn Met Asn Leu Glu Gly Gly
          40

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly Asp Ser Gly
          -30          -25          -20

Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn Gln Val Leu
          -15          -10          -5

Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His
  1          5          10          15

Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr Ile Glu Leu
          20          25          30

```

Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr
 35 40 45
 Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa Val His Asp
 50 55 60
 Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp Ser Leu Glu
 65 70 75
 Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val
 80 85 90

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly
 -30 -25 -20
 Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu
 -15 -10 -5 1
 Trp Leu Leu Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile
 5 10 15
 Gly Gln Phe Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg
 20 25 30
 Leu Met Ile Arg Lys Leu Val Ala Glu Asn Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
-25 -20 -15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
25 30 35

Cys Ala Arg
40

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys
-30 -25 -20

Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala

-15

-10

-5

1

Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
5 10 15

Ser Val Leu Lys Leu His His Ser Arg Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq SLAAALTLHGHWG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Asp Tyr Ser Leu Ala Ala Ala Leu Thr Leu His Gly His Trp Gly
-15 -10 -5

Leu Gly Gln Val Val Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7
seq LSLXASYIFGISG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
  -70                      -65                      -60
Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
  -55                      -50                      -45
Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
  -40                      -35                      -30                      -25
Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
  -20                      -15                      -10
Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
  -5                      1                      5
Arg Asn Glu Phe Val Arg Gln Ser
  10                      15

```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -76..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7
seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
  -75                      -70                      -65
Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
  -60                      -55                      -50                      -45
Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
  -40                      -35                      -30
Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Xaa Leu
  -25                      -20                      -15

```


Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq SVMGVCLLPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Trp Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu
 -20 -15 -10

Leu Ile Pro Gly Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg
 -5 1 5 10

Gly Lys Glu Lys Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met
 15 20 25

Glu Arg Asp Arg Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys
 30 35 40

Gly Pro Gly
 45

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -46..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Glu Phe Lys Leu Glu Ala His Arg Ile Val Ser Ile Ser Leu Gly
 -45 -40 -35
 Lys Ile Tyr Asn Ser Arg Val Gln Arg Gly Gly Ile Lys Leu His Lys
 -30 -25 -20 -15
 Asn Leu Leu Val Ser Leu Val Leu Arg Xaa Pro Ala Lys Ser Thr Arg
 -10 -5 1
 Ala Gly

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -97..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq IASGLGLXLDCT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
 -95 -90 -85
 Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
 -80 -75 -70
 Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
 -65 -60 -55 -50
 Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
 -45 -40 -35
 Leu Glu Val Tyr Pro Xaa Phe Leu Phe Phe Leu Ala Val Gly Gly Val
 -30 -25 -20
 Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Xaa Leu Asp Cys Trp
 -15 -10 -5

Thr Ser Ser Leu Cys Leu Trp Leu Leu His Gly Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq RIPSPLPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala
-40 -35 -30
Met Ser Ser Trp Ala Arg Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro
-25 -20 -15
Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp
-10 -5 1

(3) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq RLLRRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser
 -15 -10 -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
 1 5 10 15

Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro
 20 25 30

Ala Arg Thr
 35

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq FLLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe Leu Leu Leu
 -25 -20 -15 -10

Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -77..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.5
 seq LEWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

```

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
  -75                      -70                      -65

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
  -60                      -55                      -50

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
  -45                      -40                      -35                      -30

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
          -25                      -20                      -15

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
      -10                      -5                      1
  
```

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
  -20                      -15                      -10

Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
  -5                      1                      5                      10

Val Tyr Tyr Arg Gly Gly Val
          15
  
```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25 -20 -15 -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20

Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VFCLLSIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Gly Trp Asp Gly Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile

-10

-5

1

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(vi) ORIGINAL SOURCE:

(D) DEVELOPMENTAL STAGE: Fetal

(ix) FEATURE:

(B) LOCATION: -118..-1

(D) OTHER INFORMATION: score 4.4

seq ILAHRLGLIPIHA/DP

-115

-110

-105

-100

-95

-90

-85

-80

-75

-70

-65

- 60

-55

-50

-45

-40

- 35

-30

- 25

-20

-15

-10

-5

17

5

10

15

20

25

30

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -77..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq FEARIALLPLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
  -75                      -70                      -65

Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
  -60                      -55                      -50

Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
  -45                      -40                      -35                      -30

Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
  -25                      -20                      -15

Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
  -10                      -5                      1

Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
  5                      10                      15

Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa Xaa Val Pro
  20                      25                      30                      35

His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
  40                      45

```

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq VLFFTGWWIIIDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp
-40 -35 -30
Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe
-25 -20 -15
Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr
-10 -5 1 5
Arg

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -44..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LVFLTFLSIPSFV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Met Thr Gln Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg
-40 -35 -30
Ile Ile Cys Ser Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu
-25 -20 -15
Val Phe Leu Thr Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn
-10 -5 1
Ile Arg Ala Glu Thr Phe Leu Gln Asn Val
5 10

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq FLTALLWRGRIPG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

```

Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
      -10                -5                      1

Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
      5                10                15

Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
      20                25                30

Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa
      35                40                45                50

Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
      55                60                65

Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Xaa
      70                75                80

Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
      85                90                95

Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
      100               105               110

Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
      115               120               125

```

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
-90 -85 -30 -75

Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly
-70 -65 -60

Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln
-55 -50 -45

Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
-40 -35 -30

Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
-25 -20 -15

Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSESES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

```

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu
      -50          -45          -40
Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val Leu Leu Pro
      -35          -30          -25
Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp Leu Leu Val
      -20          -15          -10
Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
      -5          1          5          10
Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
      15          20          25
Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
      30          35          40
Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys His Arg Xaa
      45          50          55
Leu His His Tyr Tyr Gly Cys
      60          65

```

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CPTCLCAPSXXWG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu Pro
      -10          -5          1
Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys Lys
      5          10          15
Ala Arg Ser
      20

```

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq AVAASAASGQAEG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 -15 -10 -5

Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
 1 5 10

Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
15 20 25

Ile Ser Arg Leu Arg
30

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SLLXRVSVTAVAA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Ala Ala Met Ser Leu Leu Xaa Arg Val Ser Val Thr Ala Val Ala

-15 -10 -5
 Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa Leu Gly Phe Gly Gly Phe
 1 5 10 15
 Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala Pro Val Arg His Ser Gly
 20 25 30
 Asp His Gly Lys Arg Leu Phe Val Ile Arg Pro Ser Arg Phe Tyr Asp
 35 40 45
 Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr Ile Ala Leu Thr Gly Ile
 50 55 60
 Pro Val Ala Xaa Phe Ile Thr Leu Val Asn Val Phe Ile Gly Gln Ala
 65 70 75
 Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val Pro Glu His Trp Glu Tyr
 80 85 90 95
 Tyr Lys His Pro Ile Ser Arg Trp Ile Ala Arg Asn Phe Tyr Asp Ser
 100 105 110
 Pro Xaa Lys Ile Tyr Glu Arg Thr Met
 115 120

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LDLLRGLPRVSLA/NL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu
 -25 -20 -15 -10
 Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly
 -5 1 5
 Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Gly Arg Lys
 10 15 20
 Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg

```

      25          30          35
Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys
 40          45          50          55
Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu
          60          65          70
Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro
          75          80          85
Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr
          90          95          100
Ile Ala Pro
    105

```

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq GILILWIIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met	Ala	Thr	Ala	Thr	Glu	Gln	Trp	Val	Leu	Val	Glu	Met	Val	Gln	Ala
-40						-35					-30				
Leu	Tyr	Glu	Ala	Pro	Ala	Tyr	His	Leu	Ile	Leu	Glu	Gly	Ile	Leu	Ile
-25					-20					-15					-10
Leu	Trp	Ile	Ile	Arg	Leu	Leu	Phe	Ser	Lys	Thr	Tyr	Lys	Leu	Gln	Glu
				-5					1				5		
Arg	Ser	Asp	Leu	Thr	Val	Lys	Glu	Lys	Glu	Glu	Leu	Ile	Glu	Glu	Trp
		10					15					20			
Gln	Pro	Glu	Pro	Leu	Val	Pro	Pro	Val	Pro	Lys	Asp	His	Pro	Ala	Leu
	25					30					35				
Asn	Tyr	Asn	Ile	Val	Ser	Gly	Pro	Pro	Ser	His	Lys	Thr	Val	Val	Asn
40					45					50					55

Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu
 60 65 70
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr
 75 80 85
 Gly Val Gly Thr Cys Gly Pro Cys
 90 95

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq QGVLFICFTCARS/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Glu Asp Pro Asn Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro
 -75 -70 -65
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa
 -45 -40 -35
 Xaa Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 -15 -10 -5 1
 Pro Ser

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

```

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
  -30                               -25                               -20
Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
  -15                               -10                               -5
Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
   1                               5                               10                               15
His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
      20                               25                               30
Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr Ser
      35                               40                               45
Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser Gln
      50                               55                               60
Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys Tyr
      65                               70                               75                               80
Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly Xaa
      85                               90                               95
Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly
      100                               105                               110

```

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -58..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

```

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
   -55                      -50                      -45

Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr Gly
   -40                      -35                      -30

Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
   -25                      -20                      -15

His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
   -10                      -5                      1                      5

Ala Tyr Leu Pro Thr Gly Lys Trp
                   10

```

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

```

Met Ala Thr Leu Thr Phe Ser Leu Arg Lys Pro Leu Gln Arg Ser Leu
   -85                      -80                      -75

Ile Arg Pro Ser His Leu Pro Leu Cys Cys Phe Asp Trp Arg Leu Ser
   -70                      -65                      -60

His Tyr Tyr Arg Leu Pro Pro Ala Val Arg Leu His Gln Gln Arg Gly
   -55                      -50                      -45

Gly Arg Pro Gly Arg Ser Ser Ala Asp His Trp His Ser Gly Val Pro
   -40                      -35                      -30                      -25

Thr Arg Ile Leu Pro Pro Ala His Arg Leu Leu Cys Ile Gln Arg Leu
   -20                      -15                      -10

```

Pro Trp Leu Leu Leu Cys Arg Gly Ile Thr Ser
 -5 1

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq PSLAAGLLFGSXA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
 -45 -40 -35

Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
 -30 -25 -20

Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Xaa
 -15 -10 -5

Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
 1 5 10 15

Gly Phe Leu Ala Ala Thr Ser Val
 20

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 515:

```
Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly  
      -15                      -10                      -5
```

```
Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln  
      1                      5                      10
```

```
Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly  
    15                20                25                30
```

```
Tyr Tyr Arg Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala  
          35                  40                  45
```

```
Gly
```

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Brain

```
(ix) FEATURE:
  (A) NAME/KEY: sig_peptide
  (B) LOCATION: -83..-1
  (C) IDENTIFICATION METHOD: Von Heijne matrix
  (D) OTHER INFORMATION: score 4
                        seq AFSFSRLLSQCRP/DC
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met	Val	Ile	Arg	Val	Tyr	Ile	Ala	Ser	Ser	Ser	Gly	Ser	Thr	Ala	Ile	
			-90					-75						-70		
Lys	Lys	Lys	Gln	Gln	Asp	Val	Leu	Gly	Phe	Leu	Glu	Ala	Asn	Lys	Ile	
		-65					-60					-55				
Gly	Phe	Glu	Glu	Lys	Asp	Ile	Ala	Ala	Asn	Glu	Glu	Asn	Arg	Lys	Trp	
	-50					-45					-40					
Met	Arg	Glu	Asn	Val	Pro	Glu	Asn	Ser	Arg	Pro	Ala	Val	Gln	Gly	Pro	
-35					-30					-25					-20	
His	Ala	Phe	Arg	Tyr	Lys	Ala	Phe	Ser	Phe	Ser	Arg	Leu	Leu	Ser	Gln	
				-15					-10					-5		

Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe Ser Gln Tyr Cys
1 5 10
Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe Phe Phe
15 20 25

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ITSSLFLGRGSA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala Pro
-40 -35 -30
Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr Ser
-25 -20 -15
Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu Leu
-10 -5 1 5
Gln Ala Arg Gly Ile
10

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly Thr
-15 -10 -5
Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe Leu
1 5 10
Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser Asp
15 20 25 30
Phe Glu Lys Val Gln Glu Arg
35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly
-15 -10 -5
Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
1 5 10
Leu

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
-10 -5 1
Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
5 10 15
Glu Xaa Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
20 25 30 35
Asp Asp Leu Pro Ala Arg Phe Gly Tyr
40

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
-25 -20 -15 -10
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
-5 1 5
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
10 15 20

Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
 25 30 35
 Xaa Xaa Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
 40 45 50 55
 Pro Phe Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq YTAVSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
 -60 -55 -50
 Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
 -45 -40 -35 -30
 Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
 -25 -20 -15
 Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
 -10 -5 1
 Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5 10 15
 Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn Gly Arg
 20 25 30 35
 Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
 40 45

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```
Met Ala Ile Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser
-30          -25          -20          -15

Lys Leu Trp Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile
          -10          -5          1

Xaa Ala Glu Pro Pro Gln Leu Asp Ile Ser
      5          10
```

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FVLGSARLGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```
Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu Asp Asp Phe Val
      -25          -20          -15

Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met Arg Pro Ala Ala
      -10          -5          1          5

Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu Pro Asn Gln Leu
```

10

15

20

Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg Val Arg Thr Ala
25 30 35

Thr

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Lys Leu Val Ser Ala Thr Ala Trp Leu Glu Glu Cys Trp Trp Ser
-15 -10 -5 1

Glu Leu Ser

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LYVPLLAVCCCLHS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu Leu Trp
 -30 -25 -20

Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys Cys Leu
 -15 -10 -5

His Ser Val Val Phe Phe
 1

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -118..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LMIALTWVGCIFM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
 -115 -110 -105

Leu Cys Glu Arg Asp Val Ser Xaa Ser Leu Arg Leu Thr Arg Ser Ser
 -100 -95 -90

Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
 -85 -80 -75

Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
 -70 -65 -60 -55

Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
 -50 -45 -40

Xaa Xaa Ile Pro Glu Thr Val Ser Leu Glu Met Leu Xaa Xaa Ala Lys
 -35 -30 -25

Asn Lys Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val
 -20 -15 -10

Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
 -5 1 5 10

His Glu Thr Leu Thr Ser Leu Xaa Leu Glu Lys Lys Ala Arg Leu
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -100..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LASSFLFTMGGLG/FI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100 -95 -90 -85

Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80 -75 -70

Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65 -60 -55

Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50 -45 -40

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35 -30 -25

Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20 -15 -10 -5

Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile
1 5 10

Pro Lys Leu Asn Arg Phe
15

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq MLVLRSGLTALA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

```

Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr
   -10                      -5                      1

Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val Arg Lys Ala
   5                      10                      15

Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile Pro Asn Leu
  20                      25                      30                      35

Ala Arg Ile Asp Lys Gln Glu Thr Arg
                   40

```

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq NIESLAWTGGTLG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

```

Met Ala Ala Pro Leu Ser Val Glu Val Glu Phe Gly Gly Gly Ala Xaa
  -35                      -30                      -25

Ser Cys Leu Thr Val Leu Arg Asn Ile Glu Ser Leu Ala Trp Thr Gly
 -20                      -15                      -10                      -5

Gly Thr Leu Gly His Pro Glu Pro Ala His Leu Asp Gln Glu Glu Phe
   1                      5                      10

Ala Lys Arg Ala Ala Xaa Val Val His Pro Gly Arg Gln Arg Ala Ala

```

15

20

25

Arg Asn Ser Gly Ala Asp Tyr Arg
30 35

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Thr His Leu Ile Glu Tyr Asp Arg His Arg Lys Ser Arg Leu Ser
-65 -60 -55 -50

Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp His Ser Arg Asn Ala
-45 -40 -35

Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro Pro Thr Val Asp Ser
-30 -25 -20

Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val Ile Phe Trp Ser Trp
-15 -10 -5

Ala Gly Leu Val
1

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -22..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Ala Ala Ala Ala Leu Gly Gln Ile Trp Ala Arg Lys Leu Leu Ser
  -20                      -15                      -10

Val Pro Trp Leu Leu Cys Gly Pro Arg Arg Tyr Ala Ser Ser Ser Phe
  -5                      1                      5                      10

Lys Ala Ala Asp Leu Gln Leu Glu Met Thr Gln Lys Pro His Lys Lys
          15                      20                      25

Pro Gly Pro Gly Glu Pro Leu Val Phe Gly Lys Thr Phe Thr Asp His
          30                      35                      40

Met Leu Met Val Glu Trp Asn Asp Lys Gly Trp Gly Gln Pro Arg Ile
          45                      50                      55

Gln Pro Phe Gln Asn Leu Thr Leu His Pro Ala Ser Ser Ser Leu His
          60                      65                      70

Tyr Ser Leu Gln Leu Phe Glu Gly
          75                      80
  
```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -38..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq CPLLLLVTNNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ala Val Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro
  -35                      -30                      -25

Glu Lys Pro Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Val
  -20                      -15                      -10
  
```

Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg
 -5 1 5 10
 Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala
 15 20 25
 Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala
 30 35 40
 Arg Xaa Lys Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val
 45 50 55
 Lys Arg Pro
 60

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPHTA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10
 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 -5 1 5 10
 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25
 Pro Leu Ser Asp Val Leu
 30

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
-85 -80 -75
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe
-70 -65 -60 -55
Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
-50 -45 -40
Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
-35 -30 -25
Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp
-20 -15 -10
Thr Ala Val Thr Ser Gly Arg Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln Arg Phe Phe Gln

```

-65          -60          -55
Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln Ala Ala Leu Glu
-50          -45          -40

Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp Ala Gln Tyr Tyr
-35          -30          -25

Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn Tyr Cys Val Ala
-20          -15          -10          -5

Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro Asn Asn Ser Thr
          1          5          10

Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu Lys Asn Tyr Ala
          15          20          25

Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
          30          35

```

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

```

Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly Tyr Ala Gln Glu Asp
-60          -55          -50          -45

Arg Glu Arg Met His Arg Asn Ile Val Ser Leu Ala Gln Asn Leu Leu
          -40          -35          -30

Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp
          -25          -20          -15

Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro
          -10          -5          1

Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu Asn Ala Ala Trp Pro
          5          10          15          20

```

Arg

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq WSPLSTRSGGTHA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
-30 -25 -20

Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys
-15 -10 -5 1

Ser Ala Ser Met Arg Gln Pro Trp
5

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SILAQVLDQSARA/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
      -50      -45      -40
Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
      -35      -30      -25
Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
      -20      -15      -10
Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
      -5              1              5              10
Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
              15              20              25
Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
              30              35              40
Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr Thr Val Arg
              45              50              55

```

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq GLVCAGLADMARP/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

```

Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
      -60      -55      -50
Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
      -45      -40      -35
Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
      -30      -25      -20
Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
      -15      -10      -5              1
Glu Lys Leu Ser Thr Ala Gln Ser Xaa Val Leu Met Ala Thr Gly Phe
              5              10              15

```

Ile Trp Ser Arg Tyr Ser
20

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Ser Asn Tyr Ser Val Ser Leu Val Gly Pro Ala Pro Trp Gly Phe
-85                               -80                               -75

Arg Leu Gln Gly Gly Lys Asp Phe Asn Met Pro Leu Thr Ile Ser Ser
-70                               -65                               -60                               -55

Leu Lys Asp Gly Gly Lys Ala Ala Gln Ala Asn Val Arg Ile Gly Asp
                               -50                               -45                               -40

Val Val Leu Ser Ile Asp Gly Ile Asn Ala Gln Gly Met Thr His Leu
                               -35                               -30                               -25

Glu Ala Gln Asn Lys Ile Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr
-20                               -15                               -10

Leu Gln Arg Ala Ser Ala Ala Pro Lys Pro Glu Pro Val Pro Val Gln
-5                               1                               5                               10

Lys Pro Thr Val Thr Ser Val Cys Ser Glu Thr Ser Gln Glu Leu Ala
                               15                               20                               25

Glu Gly Gln Arg Arg Gly Ser Gln Gly Asp Ser Lys Gln Gln Asn
                               30                               35                               40

```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEAG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
-15 -10 -5

Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
1 5 10

Lys Glu Leu Gln Gln
15

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -40..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALLCTLLLFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ile Ile Pro Leu Leu Glu Ile Leu Ile Ile Ile Val Leu Asn Glu
-40 -35 -30 -25

Val Leu Leu Phe Asp Val Asn Ser Val Tyr Lys Ala Leu Leu Cys Thr
-20 -15 -10

Leu Leu Leu His Phe Gln Asn Ile Arg Arg Phe Leu Ser Ser Gln Ser
-5 1 5

Pro Met Lys Ala Val Ser Leu Leu Xaa Phe His Gln Pro Asp Phe Asp

10

15

20

Tyr Ile
25

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro Pro Ser Ala Thr Pro
-50 -45 -40

Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His Ser Thr Ala Arg Ile
-35 -30 -25

Val Met Pro Leu His Tyr Ser Leu Val Phe Ile Ile Gly Leu Val Gly
-20 -15 -10 -5

Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn Arg Lys Lys Ile Asn
1 5 10

Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe
15 20 25

Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met Xaa Trp Ala Leu Thr
30 35 40

Gly Glu Ser Glu Met Trp
45 50

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Pancreas

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser
-25 -20 -15

Ser Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile
-10 -5 1

Gln Gln Arg
5

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(21) International Application Number: PCT/IB98/01222 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,135 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DÜCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Régimbeau, 26, Avenue Kléber, F-75116 Paris (FR).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 8 April 1999 (08.04.99)
(54) Title: 5'ESTs FOR NON TISSUE SPECIFIC SECRETED PROTEINS (57) Abstract The sequences of 5'ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5'ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5'ESTs. The 5'ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5'ESTs. The 5'ESTs may also be used to design expression vectors and secretion vectors.		

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INTERNATIONAL SEARCH REPORT

International Application No

PC1, B 98/01222

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 98 45437 A (GENETICS INSTITUTE INC. (US); JACOBS K. ET AL.) 15 October 1998 Seq.ID:262 is 97% identical to Seq.ID:38 see page 56 - page 57 see page 63, line 9-17 ---	1-11, 15-37
X	TAKAHASHI N. ET AL.: "Periodicity of leucine and tandem repetition of a 24-amino acid segment in the primary structure of leucine-rich alpha2-glycoprotein of human serum" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA, vol. 82, April 1985, pages 1906-1910, XP002083674 see page 1908; figure 1 --- -/--	1-37



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Date of the actual completion of the international search

9 November 1998

Date of mailing of the international search report

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Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Macchia, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01222

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EMBL Emest8, Entry HS1227154 Accession number AA429129 25 May 1997 100% identity with Seq.ID:38 nt.16-64 XP002083675 see the whole document ---	3-8, 15-37
A	YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator" GENE, vol. 163, 1995, pages 193-196, XP002053953 see abstract ---	12,13
A	LIN Y. ET AL.: "Inhibition of nuclear translocation of transcription factor NF-kB by a synthetic peptide containing a cell membrane-permeable moti and nuclear localization sequence" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 24, 16 June 1995, pages 14255-14258, XP002050723 cited in the application see abstract ---	14
A	WO 96 34981 A (GENSET (FR); NICOLAEVNA MERENKOVA I.; DUMAS MILNE EDWARDS J.-B.G.) 7 November 1996 cited in the application ---	
A	KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application ---	
A	EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 cited in the application ---	
A	CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996, pages 327-336, XP002081729 cited in the application ---	
A	WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 ---	
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 98/01222

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993, pages 600-603, XP000673204	
A	HEIJNE VON G.: "A new method for predicting signal sequence cleavage sites" NUCLEIC ACIDS RESEARCH, vol. 14, no. 11, 1986, pages 4683-4690, XP002053954 cited in the application	

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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-37 all partially (Invention 1. on continuation-sheet)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Invention 1: Claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:292, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

2. Claims: Inventions 2-254: Claims 1-37 all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-291, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 293, invention 3 is limited to Seq.ID:40 and 294,....., invention 254 is limited to Seq.ID:291 and 545).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

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Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9845437 A	15-10-1998	AU 6956798 A	30-10-1998
WO 9634981 A	07-11-1996	FR 2733765 A	08-11-1996
		FR 2733762 A	08-11-1996
		AU 5982996 A	21-11-1996
		CA 2220045 A	07-11-1996
		EP 0824598 A	25-02-1996
EP 0625572 A	23-11-1994	JP 6153953 A	03-06-1994
		WO 9408001 A	14-04-1994
		US 5597713 A	28-01-1997
WO 9707198 A	27-02-1997	US 5707829 A	13-01-1998
		AU 6712396 A	18-02-1997
		AU 6768596 A	12-03-1997
		CA 2227220 A	06-02-1997
		CA 2229208 A	27-02-1997
		EP 0839196 A	06-05-1998
		EP 0851875 A	08-07-1998
		WO 9704097 A	06-02-1997